

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F69735
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-213 <KUN>
A:Cross-references: UNIPARC:UPI00000336C9; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CA
A:Experimental source: strain 168
C:Genetics:
A:Gene: xynA
A:Map position: 175 degrees
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:106/Active site: Glu #status experimental
F:200/Active site: Glu #status predicted

Query Match 100.0%; Score 1171; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.4e-80;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNSVWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNSVWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYPRTG 120

Qy 121 TYKGTVKSDDGTIDYITTYRINAPSIDGRTFTFYQWVSRQSKRPTGSNAITTFNSHVNA 180
Db 121 TYKGTVKSDDGTIDYITTYRINAPSIDGRTFTFYQWVSRQSKRPTGSNAITTFNSHVNA 180

Qy 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTVW 213

RESULT 2
S01734
endo-1,4-beta-xylanase (BC 3.2.1.8) A precursor (validated) - *Bacillus circulans*
N:Alternate names: xylanase A
C:Species: *Bacillus circulans*
C:Date: 07-Jun-1990 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
R:Yang, R.C.A.; MacKenzie, C.R.; Narang, S.A.
Nucleic Acids Res. 16, 7187, 1988
A:Title: Nucleotide sequence of a *Bacillus circulans* xylanase gene.
A:Reference number: S01734; MUID:88303346; PMID:3405767
A:Accession: S01734
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-213 <YAN>
A:Cross-references: UNIPROT:P09850; UNIPARC:UPI0000034D1C; EMBL:X07723; NID:g39462; PIDN
A:Note: part of this sequence, including the amino end of the mature protein, was confir
R:Wakarchuk, W.W.; Campbell, R.L.; Sung, W.L.; Bavoodi, J.; Yeguchi, M.
Protein Sci. 3, 467-475, 1994
A:Title: Mutational and crystallographic analyses of the active site residues of the Bac
A:Reference number: A53181; MUID:94290322; PMID:8019418
A:Contents: annotation; X-ray crystallography, 1.49 angstroms, residues 29-213
R:Campbell, R.L.
submitted to the Brookhaven Protein Data Bank, June 1994
A:Reference number: A52866; PDB:1XNB
A:Contents: annotation; X-ray crystallography, 1.49 angstroms, residues 29-213
C:Genetics:
A:Gene: xlnA

C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:97,108,140/Binding site: substrate (Tyr, Tyr, Arg) #status experimental
F:106,200/Active site: Glu #status experimental

Query Match 99.7%; Score 1168; DB 1; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.9e-80;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNSVWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNSVWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYPRTG 120

Qy 121 TYKGTVKSDDGTIDYITTYRINAPSIDGRTFTFYQWVSRQSKRPTGSNAITTFNSHVNA 180
Db 121 TYKGTVKSDDGTIDYITTYRINAPSIDGRTFTFYQWVSRQSKRPTGSNAITTFNSHVNA 180

Qy 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTVW 213

RESULT 3
S48126
endo-1,4-beta-xylanase (BC 3.2.1.8) S precursor - *Bacillus* sp. (strain YA-14)
N:Alternate names: xylanase S
C:Species: *Bacillus* sp.
A:Variety: strain YA-14
C:Date: 14-Jul-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: S48126
R:Ju-Hyun, Y.; Park, Y.S.; Yum, D.Y.; Kim, J.M.; Kong, I.S.; Bai, D.H.
J. Microbiol. Biotechnol. 3, 139-145, 1993
A:Title: Nucleotide sequence and analysis of a xylanase gene (xyns) from alkali-tolerant
A:Reference number: S48126
A:Accession: S48126
A:Molecule type: DNA
A:Residues: 1-213 <JUH>
A:Cross-references: UNIPROT:Q59256; UNIPARC:UPI0000060D47; EMBL:X59058; NID:g458800; PID
A:Experimental source: strain YA-14
C:Genetics:
A:Gene: xynS
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-213/Product: endo-1,4-beta-xylanase S #status predicted <MAT>
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>
F:106,200/Active site: Glu #status predicted

Query Match 99.5%; Score 1165; DB 1; Length 213;
Best Local Similarity 99.1%; Pred. No. 6.6e-80;
Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNSVWNSN 60
Db 1 MFKEKQFLVGLSAAALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNSVWNSN 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYPRTG 120


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QY 121 TYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNATITFSNHVNA 180

QY 181 WKSHGMNLGNNWAYQVMATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGNNWAYQVLATEGYQSSGSSNVTVM 213

RESULT 4
C83762
endo-1,4-beta-xylanhydrolase BH0899 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C83762
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C83762
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <STO>
A:Cross-references: UNIPROT:O9KEP3; UNIPARC:UPI00000DCBD1; GB:AP001510; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0899
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 73.8%; Score 864.5; DB 2; Length 210;
Best Local Similarity 74.2%; Pred. No. 1.6e-57;
Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSN 60
Db 1 MFKFTVKLTIVVIATISFCLSAVPASA--NTYQWYTDGGTVNATNGPGGNSYVTRD 58

QY 61 TGNFVVGKWTGSPRTINYNAGVWAPNGNGYLTYGWTRSPLEYVVDGSGTYRPTG 120
Db 59 TGNFVVGKWEIGSPRTIHYNAGVWEPGNGYLTYGWTRNQLIEYVVDGSGTYRPTG 118

QY 121 TYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNATITFSNHVNA 180
Db 119 THRGTVVSDGGTYDYITTRYNAPSIDGQ--TFQQFWSVRQSKRPTGNVTSITFSNHVNA 177

QY 181 WKSHGMNLGNNWAYQVMATEGYQSSGSSNVTVM 213
Db 178 WENAGMNLGSSWSYQVLATEGYQSSGSSNVTVM 210

RESULT 5
T37005
endo-1,4-beta-xylanase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37005
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21618
A:Accession: T37005
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-241 <OLI>
A:Cross-references: UNIPROT:Q9RI72; UNIPARC:UPI00000DB349; EMBL:AL109949; PIDN:CAB52919.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: xinc; SCOE:SCU11.34c
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 55.6%; Score 651.5; DB 2; Length 241;
Best Local Similarity 58.4%; Pred. No. 1.3e-41;
Matches 129; Conservative 25; Mismatches 50; Indels 17; Gaps 6;
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QY 5 KKNFLVG--LSAALMSISLFSATASAST-----DYQWNTDGGGIVNAVNGSG 51
Db 23 RRGFLGGAGTALATASGLLLPGTAHAATTTTNTGTDGMYISFTWTDGGSVMTLNGG 82

QY 52 GNYSVNWSNTGNFVVGKWTGSPRTINYNAGVWAPNGNGYLTYGWTRSPLEYVVD 111
Db 83 GSYSYQWNTNCGNFVAGKCGWSTGGR--RTVRYN--GYFNPSCNGYGCYLGWTSNPLVEYIYD 140

QY 112 SWGTYRPTGTYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNAT 171
Db 141 NMGYSYRPTGTYKGTVSSDGGTYDYITTRYNAPSVEGK--TFQQYWSVRQSKVTSGS--GT 198

QY 172 ITFSNHVNAWKSHGMNLGNNWAYQVMATEGYQSSGSSNVTVM 212
Db 199 ITTGNHFDPAWARAGNMCGFRYYIMATEGYQSSGSSNITV 239

RESULT 6
JS0591
endo-1,4-beta-xylanase (EC 3.2.1.8) C precursor - Streptomyces lividans
N:Alternate names: xylanase C
C:Species: Streptomyces lividans
C:Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: JS0591; PS0240
R:Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A:Reference number: JS0589; MUID:92077439; PMID:1743521
A:Accession: JS0591
A:Molecule type: DNA
A:Residues: 1-240 <SHA>
A:Cross-references: UNIPROT:P26220; UNIPARC:UPI0000034D31; GB:M64553; NID:G153530; PIDN
A:Accession: PS0240
A:Molecule type: protein
A:Residues: 50-80 <SH2>
A:Cross-references: UNIPARC:UPI00000172965
C:Genetics:
A:Gene: xinc
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-49/Domain: signal sequence #status predicted <SIG>
F:50-240/Product: endo-1,4-beta-xylanase C #status experimental <MAT>
F:62-239/Domain: endo-1,4-beta-xylanase homology <XYL>
F:134,226/Active site: Glu #status predicted

Query Match 54.4%; Score 637; DB 1; Length 240;
Best Local Similarity 57.5%; Pred. No. 1.6e-40;
Matches 127; Conservative 24; Mismatches 52; Indels 18; Gaps 6;

QY 5 KKNFLVG--LSAALMSISLFSATASAST-----DYQWNTDGGGIVNAVNGSG 51
Db 23 RRGFLGGAGTALATASGLLLPGTAHAATTTTNTGTDGMYISFTWTDGGSVMTLNGG 82

QY 52 GNYSVNWSNTGNFVVGKWTGSPRTINYNAGVWAPNGNGYLTYGWTRSPLEYVVD 111
Db 83 GSYSYQWNTNCGNFVAGKCGWSTGD--GNVRYN--GYFNPVNGYGCYLGWTSNPLVEYIYD 139

QY 112 SWGTYRPTGTYKGTVKSDGGTYDYITTRYNAPSIDGDRITFTQVWSVRQSKRPTGNSNAT 171
Db 140 NMGYSYRPTGTYKGTVSSDGGTYDYITTRYNAPSVEGK--TFQQYWSVRQSKVTSGS--GT 197

QY 172 ITFSNHVNAWKSHGMNLGNNWAYQVMATEGYQSSGSSNVTVM 212
Db 198 ITTGNHFDPAWARAGNMCGFRYYIMATEGYQSSGSSNITV 239

RESULT 7
S47512
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - Streptomyces sp.
N:Alternate names: xylanase
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Qy 93 YLTLYGWTSPLEIYYVVDSWGVTYRPTGYKGTGVDYDITTTTRYNAPSIDGDRTT 152
Db 115 YLALYGTWNPLVEYYIVDNGWGTYRPTGEGYKGTVTSDGGTYDITKTRVNKNPVEGTR-T 173

Qy 153 FTOYWSVROSKRPTGSNATITFNSHNHNAWKSHGMNLGNSWAYQVMATEGYQSSGSSNVTV 212
Db 174 FDOYWSVRQAKRTGG---TITGNGHFDANARAGKPLGNFSYNYMIMATEGYQSSGSSINV 230

RESULT 12
JC7577
N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7577; PC7120
R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.
BioSci. Biotechnol. Biochem. 64, 2734-2738, 2000
A;Title: Molecular cloning, overexpression, and purification of a major xylanase
A;Reference number: JC7577; PMID: 21077500; PMID:11210150
A;Accession: JC7577
A;Molecule type: DNA
A;Residues: 1-232 <KIM>
A;Cross-references: UNIPROT:Q9HF44; UNIPARC:UPI0000069976; DDBJ:AB044941
A;Experimental source: strain KBN616
A;Accession: PC7120
A;Molecule type: protein
A;Residues: 45-64 <KI2>
A;Cross-references: UNIPARC:UPI0000175A84
C;Comment: This enzyme has strong similarity to other fungal family 11 endoxylanase
C;Genetics:
A;Gene: xynG2
A;Introns: 100/2
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase

Query Match 49.4%; Score 578; DB 2; Length 232;
Best Local Similarity 52.1%; Pred. No. 3.8e-36;
Matches 122; Conservative 31; Mismatches 47; Indels 34; Gaps 9;

Qy 7 NFIIVGLSALMSIS-----LFSATA-----SAASTD-----YWNQWTDGG 41
Db 6 SILLACSAAGALATPIEPLADHPNFAFETAFLVGRSTPSTGYNNGYYSFVTDGG 65

Qy 42 GIVNAVNGSGGNSVNWNSMTGNFVVGKGTGTTSPFRTINYNAGVAPNGNGYILTYGWTR 101
Db 66 GDVYTINGGGSISVQWSNNGFVVGKGNWPGSS-RAIYY-SGSFNPNGNYLAVYGWTT 123

Qy 102 SPLIEYYVVDSWGVTYRPT--TGTYKGTGKSDGGTYDITTTTRYNAPSIDGDRTTFTQWSV 159
Db 124 DPLIEYYIVESYGTNPYNGSGTYKGVQVTSDDGGTYNIVTSVRTNAPSIIG-TATFTQFSV 182

Qy 160 ROSKRPTGSNATITFNSHNHNAWKSHGMNLGNSWAYQVMATEGYQSSGSSNVTVW 213
Db 183 RTSKRVG---TVTTGNGHFNAAKYGLTLGTH-NYQIVATEGYQSSGSSAITVY 232

RESULT 13
S57469
N;Alternate names: xylanase 2
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: S57469
R;Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A;Description: Expression in Saccharomyces cerevisiae of two xylanase encoding
A;Reference number: S57469
A;Accession: S57469
A;Molecule type: DNA
A;Residues: 1-221 <PER>
A;Cross-references: UNIPROT:P55333; UNIPARC:UPI0000139075; EMBL:Z49893; NID:987
C;Genetics:

```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:04:18 ; Search time 199 Seconds
(without alignments)
470.290 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171

Sequence: 1 MFKPKNKLVLGLSALMSIS.....YQVMATEGYQSSGSSNTVTW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	3	Aay93752 A bacteri
2	1171	100.0	213	7	Adc27541 Bacillus
3	1171	100.0	213	7	Ado55909 Bacillus
4	1171	100.0	213	8	Adj34972 Xylanase
5	1168	99.7	213	3	Aab48532 Bacillus
6	1168	99.7	213	3	Aab48518 Bacillus
7	1168	99.7	213	5	Aao18638 B subtili
8	1168	99.7	213	5	Aao18624 Endo-1,4-
9	1168	99.7	213	8	Adj35008 Xylanase
10	1168	99.7	213	8	Adi66728 B. circul
11	1168	99.7	213	8	Adi66740 B. subtil
12	1161	99.1	213	3	Aay93755 A bacteri
13	1154	98.5	213	3	Aay93753 A bacteri
14	1149	98.1	213	3	Aay93754 A bacteri
15	1130	96.5	213	2	Aar47200 Modified
16	1130	96.5	213	3	Aay93751 A bacteri
17	1125	96.1	213	8	Ado70164 Xylanase,
18	1104	94.3	213	8	Adj35014 Xylanase
19	1097	93.7	213	8	Adj35086 Xylanase
20	1041	88.9	185	2	Aaw60732 Xylanase
21	1041	88.9	185	3	Aay98064 B. subtil
22	1041	88.9	185	4	Aab69043 B. subtil
23	1041	88.9	185	4	Aau07391 Bacillus
24	1041	88.9	185	5	Aae18441 Bacillus

25	1041	88.9	185	7	Adc27530	Bacillus
26	1041	88.9	197	8	Adh10230	Xylanase
27	1041	88.9	353	4	Aab69045	Xylanase
28	1041	88.9	360	8	Adh10231	Xylanase
29	1038	88.6	185	2	Aaw60730	Xylanase
30	1038	88.6	185	3	Aay98062	B. circul
31	1038	88.6	185	5	Aao18625	B. circul
32	1038	88.6	185	5	Aae18439	Bacillus
33	1034	88.3	353	4	Aab69046	NL-xylana
34	1033	88.2	185	2	Aaw60279	Modified
35	1030	88.0	185	2	Aaw60278	Modified
36	987	84.3	185	3	Aab48524	Xylanase
37	987	84.3	185	3	Aab48523	Xylanase
38	987	84.3	185	5	Aao18629	Modified
39	987	84.3	185	5	Aao18630	Modified
40	987	84.3	185	8	Adi66732	B. circul
41	984	84.0	185	3	Aab48528	Xylanase
42	984	84.0	185	5	Aao18634	Modified
43	984	84.0	185	8	Adi66736	B. circul
44	979	83.6	185	3	Aab48526	Xylanase
45	979	83.6	185	5	Aao18632	Modified

ALIGNMENTS

RESULT 1

AAy93752
ID AAY93752 standard; protein; 213 AA.
XX
AC AAY93752;
XX
DT 03-OCT-2000 (first entry)
XX
DE A bacterial endo-beta-1,4-xylanase protein.
XX
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
KW dough; dough preparation.
XX
OS Bacillus subtilis.
XX
PN WO200039289-A2.
XX
PD 06-JUL-2000.
XX
PF 17-DEC-1999; 99WO-IB002071.
XX
PR 23-DEC-1998; 98GB-00028599.
PR 06-APR-1999; 99GB-00007805.
PR 15-APR-1999; 99GB-00008645.
(DANI-) DANISCO AS.
Sibbesen O, Sorensen JF;
WPI; 2000-465744/40.
N-PSDB; AAA47154.
Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.

Claim 10; Page 108; 112pp; English.

The present sequence represents an endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the

inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample

Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.8e-91;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGNYSVNWNS 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGNYSVNWNS 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTVDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTVDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213

RESULT 2
ADC27541
ID ADC27541 standard; protein; 213 AA.
XX AC ADC27541;
XX DT 18-DEC-2003 (first entry)
XX DE Bacillus subtilis wild-type xylanase enzyme.
XX KW xylanase; xylanase inhibitor; thermosensitivity; plant cell wall;
KW plant material; baking; processing cereal; starch production;
KW processing wood; wood pulp bleaching; animal feed; flour separation;
KW wetmilling; paper and pulp production; flour dough; hemicellulose;
KW arabinoxylan; food supplement; xylan; baking process; bread volume;
KW crumb structure; crumb appearance; shelf-life; enzyme.
XX OS Bacillus subtilis.
XX PN WO2003020923-A1.
XX PD 13-MAR-2003.
XX PF 30-AUG-2002; 2002WO-IB003797.
XX PR 04-SEP-2001; 2001GB-00021387.
XX PA (DANI-) DANISCO AS.
XX PI Sibbesen O, Sorensen JF;
XX DR WPI; 2003-332934/31.
XX DR N-PSDB; ADC27538.
XX PT Novel variant xylanase polypeptide having altered sensitivity to a
PT xylanase inhibitor and altered thermosensitivity as compared with a
PT parent xylanase enzyme, useful in baking, processing cereals, starch
PT production.
XX PS Disclosure; Fig 1; 63pp; English.
XX CC This invention relates to a novel variant xylanase protein or its
CC fragment having xylanase activity. the variants have one or more amino
CC acid modifications so that the protein or fragment has an altered
CC sensitivity to a xylanase inhibitor and has an altered thermosensitivity
CC as compared with a parent xylanase enzyme. The variant xylanases of the
CC invention are useful for degrading or modifying a plant cell wall, and

for processing a plant material. They may be useful for baking, processing cereals, starch production, in processing wood, and enhancing the bleaching of wood pulp. They may also be useful for a variety of applications such as animal feed, flour separation (wetmilling) and paper and pulp production. In addition, they may also be useful for preparing a flour dough. The enzymes of the invention may alter or reduce the viscosity derived from the presence of hemicellulose or arabinoxylan in a solution or system comprising plant cell wall material, and for modifying food and/or feed supplement comprising xylan. Use of the variant xylanases in baking processes improves the properties of flour based doughs and products made from the doughs. The baked products have highly desirable characteristics with respect to blood volume, crumb structure and appearance and additionally have an extended shelf-life. The enzymes of the invention have reduced thermosensitivity and inhibitor sensitivity, which allows a reduction in the amount of xylanase required for animal feed, starch production and baking. The present sequence is that of the full-length wild-type *Bacillus subtilis* xylanase which was used to create the variant xylanases of the invention.

Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.8e-91;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGNYSVNWNS 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGNYSVNWNS 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTVDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTVDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213

RESULT 3
ADO55909
ID ADO55909 standard; protein; 213 AA.
XX AC ADO55909;
XX DT 15-JUL-2004 (first entry)
XX DE Bacillus subtilis xynA protein sequence SeqID4.
XX KW cellulase; microorganism; organic fertiliser; faeces; urine;
KW domestic animal; sawdust; pLYH7-39; bgIC; xylanase; pLYH8-49; xynA;
KW pLYH8-62; xynD; pectate lyase; pLYH9-24; pella; pLYH9-46; pelB;
KW fermentation; enzyme.
XX OS Bacillus subtilis.
XX PN KR2003015943-A.
XX PD 26-FEB-2003.
XX PF 18-AUG-2001; 2001KR-00049794.
XX PR 18-AUG-2001; 2001KR-00049794.
XX PA (KOBI-) KOREA BIO FERTILIZER CO LTD.
XX PI Lee YH, Yoon HJ;
XX DR WPI; 2003-455433/43.
XX DR N-PSDB; ADO55908.

XX Gene encoding cellulase, cellulase expressed by the same, microorganism
 PT containing the same gene, and organic fertilizer using the same
 PT microorganism.
 XX
 PS Claim 2; SEQ ID NO 4; Jpp; Korean.
 XX
 CC This invention relates to novel genes encoding cellulase, cellulase
 CC expressed by the same, a microorganism containing the same gene, and an
 CC organic fertilizer using the same microorganism, therefore the organic
 CC fertilizer can be rapidly produced from a mixture of the faeces and urine
 CC of domestic animals and sawdust. The microorganism *Bacillus subtilis*
 CC contains one cellulase encoding gene pLVH7-39(bg1C), two xylanase
 CC encoding genes pLVH8-24(kyNA) and pLVH8-62(kyND) and two pectate lyase
 CC encoding genes pLVH9-44(pelA) and pLVH9-46(pelB). The organic fertilizer
 CC is produced by inoculating an appropriate amount of the microorganism
 CC *Bacillus subtilis* into the mixture of the faeces and urine of domestic
 CC animals and sawdust and fermenting the mixture. The present sequence is
 CC that of a *Bacillus subtilis* protein which is related to the production of
 CC the organic fertilizer of the invention.
 XX
 SQ Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFKEKKNFLVGLSALMSISLFSATASAASDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
 Db 1 MFKEKKNFLVGLSALMSISLFSATASAASDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
 Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
 Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
 Qy 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRFTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
 Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRFTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
 Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
 Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 4
 ADJ34972
 ID ADJ34972 standard; protein; 213 AA.
 AC ADJ34972;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Xylanase from an environmental sample seq id 188.
 XX
 KW antibacterial; fungicide; thermostable xylanase activity;
 KW dough conditioning; beverage production; nutritional supplement;
 KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
 KW fungal infection; coccidiosis.
 XX
 OS Unidentified.
 XX
 XX WO2003106654-A2.
 XX
 XX 24-DEC-2003.
 XX
 XX 16-JUN-2003; 2003WO-US019153.
 XX
 XX 14-JUN-2002; 2002US-0389299P.
 XX
 XX (DIVE-) DIVERSA CORP.
 XX
 XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
 PI Esteghlalian A;

XX WPI; 2004-099016/10.
 DR N-PSDB; ADJ34971.
 XX
 PT Novel xylanase recombinant polypeptide useful for improving textile
 PT texture, treating paper, eliminating microorganisms.
 XX
 PS Claim 60; SEQ ID NO 188; 570pp; English.
 XX
 CC The invention describes an isolated or recombinant polypeptide (I),
 CC having 50% or more identity to 190 300-1200 residue amino acid sequences
 CC (SI), given in the specification, over a region of 100 or more residues
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
 CC dough conditioning; beverage production; as a nutritional supplement in
 CC animal feed; reducing lignin in a wood or a wood product; and for
 CC eliminating and protecting animals from a microorganism comprising xylan.
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
 CC acid encoding a polypeptide having a xylanase activity which involves
 CC amplification of a template nucleic acid with a primer pair capable of
 CC amplifying (II) or its subsequence. (I) is useful for treating and
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.
 CC This is the amino acid sequence of a xylanase protein isolated from an
 CC environmental sample.
 XX
 SQ Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 8; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFKEKKNFLVGLSALMSISLFSATASAASDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
 Db 1 MFKEKKNFLVGLSALMSISLFSATASAASDYQWNTDGGGIYVNAVNGSGNYSVNWSN 60
 Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
 Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
 Qy 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRFTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
 Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRFTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
 Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
 Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 5
 AAB48532
 ID AAB48532 standard; protein; 213 AA.
 XX
 AC AAB48532;
 XX
 DT 05-MAR-2001 (first entry)
 XX
 DE *Bacillus subtilis* xylanase.
 XX
 KW Bacterial; *Bacillus circulans*; xylanase; xylanase activity; XA;
 KW bleaching agent.
 XX
 OS *Bacillus subtilis*.
 XX
 XX WO200068396-A2.
 XX
 XX 16-NOV-2000.
 XX
 XX 12-MAY-2000; 2000WO-US013172.
 XX
 XX 12-MAY-1999; 99US-0133714P.
 XX
 XX (XENC-) XENCOR INC.
 XX
 XX Bentzien JM;

XX WPI; 2000-679800/66.
XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX
PS Disclosure; Fig 16A; 114pp; English.
XX
XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 213 AA;
Query Match 99.7%; Score 1168; DB 3; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNQWTDGGGIYNAVNGSGGYSVNWNS 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNQWTDGGGIYNAVNGSGGYSVNWNS 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFTNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFTNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
RESULT 6
AAB48518
ID AAB48518 standard; protein; 213 AA.
XX
AC AAB48518;
XX
DT 05-MAR-2001 (first entry)
XX
XX Bacillus circulans endo-1,4-beta xylanase precursor.
XX
KW Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent.
XX
OS Bacillus circulans.
XX
PN WO200068396-A2.
XX
PD 16-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US013172.
XX
XX 12-MAY-1999; 99US-0133714P.
XX
XX (XENC-) XENCOR INC.
XX
XX Bentzien JM;
XX
XX WPI; 2000-679800/66.
XX
XX Non naturally occurring XA protein with enhanced thermophilicity,
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX
PS Disclosure; Fig 1A; 114pp; English.

XX
CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermophilicity, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp
XX
SQ Sequence 213 AA;
Query Match 99.7%; Score 1168; DB 3; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNQWTDGGGIYNAVNGSGGYSVNWNS 60
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASASTDYQNQWTDGGGIYNAVNGSGGYSVNWNS 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFTNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFTNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
RESULT 7
AAO18638
ID AAO18638 standard; protein; 213 AA.
XX
AC AAO18638;
XX
DT 24-OCT-2002 (first entry)
XX
XX B subtilis xylanase.
XX
DE Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutein.
XX
XX Bacillus subtilis.
XX
OS WO200238746-A2.
XX
PN 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US048018.
XX
XX 10-NOV-2000; 2000US-00710050.
XX
XX (XENC-) XENCOR INC.
XX
XX Bentzien J, Dahiyat B;
XX
XX WPI; 2002-608200/65.
XX
XX Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
XX Disclosure; Fig 16A; 121pp; English.
XX
XX The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermostability,
CC alkalophilicity, or thermostability relative to naturally occurring B.

CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNFVLGLSALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYVNWNSN 60
DB 1 MFKFKNFVLGLSALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYVNWNSN 60
QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYPRTG 120
QY 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
QY 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTW 213

RESULT 8
AAO18624
ID AAO18624 standard; protein; 213 AA.
AC AAO18624;
XX
XX
DT 24-OCT-2002 (first entry)
XX
DE Endo-1,4-beta xylanase precursor protein.
XX
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KW liquid clarification; coffee extraction; plant oil extraction;
KW starch extraction; food thickener; animal food additive; mutant; mutein.
XX
OS Unidentified.
XX
PN WO200238746-A2.
XX
PD 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US048018.
PF
XX 10-NOV-2000; 2000US-00710050.
PR
XX (XENC-) XENCOR INC.
PA
XX Bentzien J, Dahiyat B;
PI
XX WPI; 2002-608200/65.
DR
XX Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
PS Disclosure; Fig 1A; 121pp; English.
XX
XC The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the

CC protein has been modified to exhibit enhanced thermophilicity,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention
XX
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNFVLGLSALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYVNWNSN 60
DB 1 MFKFKNFVLGLSALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYVNWNSN 60
QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYPRTG 120
QY 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
QY 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGNSWAYQVMATEGYQSSGSSNVTW 213

RESULT 9
ADJ35008
ID ADJ35008 standard; protein; 213 AA.
XX
XX AC ADJ35008;
XX
DT 22-APR-2004 (first entry)
XX
XX Xylanase from an environmental sample seq id 224.
DE
XX antibacterial; fungicide; thermostable xylanase activity;
KW dough conditioning; beverage production; nutritional supplement;
KW animal feed; lignin reduction; wood product; xylan; bacterial infection;
KW fungal infection; coccidioides.
XX
OS Unidentified.
XX
PN WO2003106654-A2.
XX
PD 24-DEC-2003.
XX
PF 16-JUN-2003; 2003WO-US019153.
XX
PR 14-JUN-2002; 2002US-0389299P.
XX
XX (DIVE-) DIVERSA CORP.
XX
XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;
PI Esteghlalian A;
XX WPI; 2004-099016/10.
DR N-PSDB; ADJ35007.
XX
XX Novel xylanase recombinant polypeptide useful for improving textile
PT texture, treating paper, eliminating microorganisms.
XX
PS Claim 60; SEQ ID NO 224; 570pp; English.

XX The invention describes an isolated or recombinant polypeptide (I),
CC having 50% or more identity to 190 300-1200 residue amino acid sequences
CC (SI), given in the specification, over a region of 100 or more residues
CC and the polypeptide as thermostable xylanase activity. (I) is useful for:
CC dough conditioning; beverage production; as a nutritional supplement in
CC animal feed; reducing lignin in a wood or a wood product; and for
CC eliminating and protecting animals from a microorganism comprising xylan.
CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic
CC acid encoding a polypeptide having a xylanase activity which involves
CC amplification of a template nucleic acid with a primer pair capable of
CC amplifying (II) or its subsequence. (I) is useful for treating and
CC preventing bacterial infection and fungal infection e.g. coccidiosis.
CC This is the amino acid sequence of a xylanase protein isolated from an
CC environmental sample.

XX SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 8; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFEPKKNFLVGLSAAALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYSVNWSN 60
Db 1 MFEPKKNFLVGLSAAALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYSVNWSN 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRFTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRFTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 10
ADI66728
ID ADI66728 standard; protein; 213 AA.

XX AC ADI66728;

XX DT 22-APR-2004 (first entry)

XX DE B. circulans endo-1,4-beta xylanase.

XX Endo-1,4-beta xylanase; XA; EC 3.2.1.8; enzyme; bleaching;
KW bleaching pulp; paper industry; food; animal feed; thermostability;
KW alkalophilic; hot alkali treatment.

XX OS Bacillus circulans.

XX FH Key Location/Qualifiers
FT Peptide 1..28
FT Protein /note= "Signal peptide"

FT 29..213
FT /note= "Mature Xylanase"

XX US6682923-B1.

XX PD 27-JAN-2004.

XX PF 12-MAY-2000; 2000US-00570856.

XX PR 12-MAY-1999; 99US-0133714P.

XX PR 07-JUN-1999; 99US-0138156P.

XX PA (XENC-) XENCOR.

XX PI Bentzien J, Dahiyat BI;

XX WPI; 2004-118575/12.
DR N-PSDB; ADI66729.

XX New mutant xylanase (XA) protein comprising at least four amino acid
PT substitutions as compared to Bacillus circulans xylanase, useful for
PT bleaching (paper) pulp, and in the food and animal feed industries.

XX Claim 2; SEQ ID NO 1; 84pp; English.

XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also
CC included is a bleaching agent comprising the XA protein. The non-
CC naturally occurring XA protein comprises at least four amino acid
CC substitutions as compared to Bacillus circulans xylanase ADI66728. The
CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
CC useful for bleaching pulp in the paper and related industries, but is
CC also useful in the food and animal feed industries. The new protein is
CC active at higher pH and temperature ranges than naturally occurring
CC xylanases, simplifying incorporation of the xylanase treatment step into
CC pulp processing, especially where the enzyme is added after hot alkali
CC treatment. The present sequence represents the wild-type xylanase.

XX SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 8; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFEPKKNFLVGLSAAALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYSVNWSN 60
Db 1 MFEPKKNFLVGLSAAALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYSVNWSN 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRFTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTTTRYNAPSIDGDRFTTFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 11

ADI66740

ID ADI66740 standard; protein; 213 AA.

XX AC ADI66740;

XX DT 22-APR-2004 (first entry)

XX DE B. subtilis xylanase.

XX Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;
KW paper industry; food; animal feed; thermostability; alkalophilic;
KW hot alkali treatment.

XX OS Bacillus subtilis.

XX PN US6682923-B1.

XX PD 27-JAN-2004.

XX PF 12-MAY-2000; 2000US-00570856.

XX PR 12-MAY-1999; 99US-0133714P.

XX PR 07-JUN-1999; 99US-0138156P.

```
PA (XENC-) XENCOR.
XX
XX Bentzien J, Dahiyat BI;
XX
XX WPI; 2004-118575/12.
XX
XX New mutant xylanase (XA) protein comprising at least four amino acid
XX substitutions as compared to Bacillus circulans xylanase, useful for
XX bleaching (paper) pulp, and in the food and animal feed industries.
XX
XX Disclosure; SEQ ID NO 13; 84pp; English.
XX
XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta
XX xylanase from Bacillus circulans) protein appearing as ADI66730. Also
XX included is a bleaching agent comprising the XA protein. The non-
XX naturally occurring XA protein comprises at least four amino acid
XX substitutions as compared to Bacillus circulans xylanase ADI66728. The
XX amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,
XX 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,
XX 58, or 144. The non-naturally occurring xylanase activity (XA) protein is
XX useful for bleaching pulp in the paper and related industries, but is
XX also useful in the food and animal feed industries. The new protein is
XX active at higher pH and temperature ranges than naturally occurring
XX xylanases, simplifying incorporation of the xylanase treatment step into
XX pulp processing, especially where the enzyme is added after hot alkali
XX treatment. The present sequence is a xylanase from another species
XX included for comparison.
XX
XX Sequence 213 AA;
SQ

Query Match 99.7%; Score 1168; DB 8; Length 213;
Best Local Similarity 99.5%; Pred. No. 3.3e-91;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKKKFLVGLSALMSISLFSATASAASTDYQWNTDGGGVNAVNGSGGYSVNWNSN 60
Db 1 MFKKKFLVGLSALMSISLFSATASAASTDYQWNTDGGGVNAVNGSGGYSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRP TGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRP TGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 12
RAY93755
ID AAY93755 standard; protein; 213 AA.
XX
XX AAY93755;
XX
XX 03-OCT-2000 (first entry)
XX
XX A bacterial endo-beta-1,4-xylanase mutant XM3.
XX
XX Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX dough; dough preparation.
XX
XX Synthetic.
XX Bacillus subtilis.
XX
XX WO200039289-A2.
XX
XX 06-JUL-2000.
XX
XX 17-DEC-1999; 99WO-IB002071.
XX
XX
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PR 23-DEC-1998; 98GB-00028599.
PR 06-APR-1999; 99GB-00007805.
PR 15-APR-1999; 99GB-00008645.
XX
XX (DANI-) DANISCO AS.
XX
XX Sibbesen O, Sorensen JF;
XX
XX WPI; 2000-465744/40.
XX N-ESDB; AAA47157.
XX
XX Mutant xylanase protein identified using xylanase inhibitor useful for
XX preparing non-sticky dough for bakery products.
XX
XX Claim 1; Page 111; 112pp; English.
XX
XX The present sequence represents a mutant endo-beta-1,4-xylanase. The
XX specification also describes an endo-beta-1,4-xylanase inhibitor, which
XX is obtained from wheat flour. The specification also describes a mutant
XX xylanase protein. The xylanase is useful for preparing a foodstuff,
XX preferably a bakery product or a substance (e.g. a dough) for making the
XX bakery product. Wild type xylanase or mutant xylanase is useful for
XX preparing a dough that is less sticky than a dough comprising a fungal
XX xylanase. The xylanase inhibitor is useful for screening high degree
XX resistance xylanases for dough preparation. The xylanase is also useful
XX for preparing a non-sticky dough. A combination of xylanase and the
XX inhibitor is useful for calibrating and/or determining the quantity of
XX inhibitor in a wheat flour sample
XX
XX Sequence 213 AA;
SQ

Query Match 99.1%; Score 1161; DB 3; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.3e-90;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKKKFLVGLSALMSISLFSATASAASTDYQWNTDGGGVNAVNGSGGYSVNWNSN 60
Db 1 MFKKKFLVGLSALMSISLFSATASAASTDYQWNTDGGGVNAVNGSGGYSVNWNSN 60

Qy 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRP TGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRP TGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 13
RAY93753
ID AAY93753 standard; protein; 213 AA.
XX
XX AAY93753;
XX
XX 03-OCT-2000 (first entry)
XX
XX A bacterial endo-beta-1,4-xylanase mutant XM1.
XX
XX Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX dough; dough preparation.
XX
XX Synthetic.
XX Bacillus subtilis.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 43 /note= "wild type Ile changed to Thr"
XX
XX Misc-difference 197 /note= "wild type Met changed to Leu"
XX
XX
```

```
FT Misc-difference 203
XX /note= "wild type Gln changed to Lys"
XX
FN W0200039289-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 17-DEC-1999; 99WO-IB002071.
XX
XX PR 23-DEC-1998; 98GB-00028599.
XX PR 06-APR-1999; 99GB-00007805.
XX PR 15-APR-1999; 99GB-00008645.
XX
XX PA (DANI-) DANISCO AS.
XX
XX PI Sibbesen O, Sorensen JF;
XX
XX DR WPI; 2000-465744/40.
XX DR N-PSDB; AAA47155.
XX
XX FT Mutant xylanase protein identified using xylanase inhibitor useful for
XX preparing non-sticky dough for bakery products.
XX
XX PS Claim 1; Page 109; 112pp; English.
XX
XX CC The present sequence represents a mutant endo-beta-1,4-xylanase. The
XX specification also describes an endo-beta-1,4-xylanase inhibitor, which
XX is obtained from wheat flour. The specification also describes a mutant
XX xylanase protein. The xylanase is useful for preparing a foodstuff,
XX preferably a bakery product or a substance (e.g. a dough) for making the
XX bakery product. Wild type xylanase or mutant xylanase is useful for
XX preparing a dough that is less sticky than a dough comprising a fungal
XX xylanase. The xylanase inhibitor is useful for screening high degree
XX resistance xylanases for dough preparation. The xylanase is also useful
XX for preparing a non-sticky dough. A combination of xylanase and the
XX inhibitor is useful for calibrating and/or determining the quantity of
XX inhibitor in a wheat flour sample
XX
XX SQ Sequence 213 AA;
XX
XX Query Match 98.5%; Score 1154; DB 3; Length 213;
XX Best Local Similarity 98.1%; Pred. No. 5.1e-90;
XX Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 MFKFKQFLVGLSAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60
XX Db 1 MFKFKQFLVGLSAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60
XX
XX Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLGWTSPLEIYYVVDWSGTYRPTG 120
XX Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLGWTSPLEIYYVVDWSGTYRPTG 120
XX
XX Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180
XX Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180
XX
XX Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVTW 213
XX Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVTW 213
XX
XX RESULT 14
XX AAY93754
XX ID AAY93754 standard; protein; 213 AA.
XX
XX AC AAY93754;
XX
XX DT 03-OCT-2000 (first entry)
XX
XX DE A bacterial endo-beta-1,4-xylanase mutant XM2.
XX
XX KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX dough; dough preparation.
XX
```

```
XX Synthetic.
XX Bacillus subtilis.
XX
XX FN W0200039289-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 17-DEC-1999; 99WO-IB002071.
XX
XX PR 23-DEC-1998; 98GB-00028599.
XX PR 06-APR-1999; 99GB-00007805.
XX PR 15-APR-1999; 99GB-00008645.
XX
XX PA (DANI-) DANISCO AS.
XX
XX PI Sibbesen O, Sorensen JF;
XX
XX DR WPI; 2000-465744/40.
XX DR N-PSDB; AAA47155.
XX
XX FT Mutant xylanase protein identified using xylanase inhibitor useful for
XX preparing non-sticky dough for bakery products.
XX
XX PS Claim 1; Page 110; 112pp; English.
XX
XX CC The present sequence represents a mutant endo-beta-1,4-xylanase. The
XX specification also describes an endo-beta-1,4-xylanase inhibitor, which
XX is obtained from wheat flour. The specification also describes a mutant
XX xylanase protein. The xylanase is useful for preparing a foodstuff,
XX preferably a bakery product or a substance (e.g. a dough) for making the
XX bakery product. Wild type xylanase or mutant xylanase is useful for
XX preparing a dough that is less sticky than a dough comprising a fungal
XX xylanase. The xylanase inhibitor is useful for screening high degree
XX resistance xylanases for dough preparation. The xylanase is also useful
XX for preparing a non-sticky dough. A combination of xylanase and the
XX inhibitor is useful for calibrating and/or determining the quantity of
XX inhibitor in a wheat flour sample
XX
XX SQ Sequence 213 AA;
XX
XX Query Match 98.1%; Score 1149; DB 3; Length 213;
XX Best Local Similarity 97.7%; Pred. No. 1.3e-89;
XX Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy 1 MFKFKQFLVGLSAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60
XX Db 1 MFKFKQFLVGLSAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60
XX
XX Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLGWTSPLEIYYVVDWSGTYRPTG 120
XX Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLGWTSPLEIYYVVDWSGTYRPTG 120
XX
XX Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180
XX Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180
XX
XX Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVTW 213
XX Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVTW 213
XX
XX RESULT 15
XX AAR47200
XX ID AAR47200 standard; protein; 213 AA.
XX
XX AC AAR47200;
XX
XX DT 25-MAR-2003 (revised)
XX DT 10-AUG-1994 (first entry)
XX
XX DE Modified xylanase of Bacillus subtilis.
XX
```

KW Xylanase; Bacillus subtilis; baking; bread; yeast; food; foodstuffs;
KW bread; pastry.

XX Bacillus subtilis.

XX Key Location/Qualifiers
XX FH Peptide 1..28
XX FT /label= Signal peptide.

FT Misc-difference 7 /note= "Wild type amino acid substituted for Lys."

FT Misc-difference 13 /note= "Wild type amino acid substituted for Thr."

FT Misc-difference 16 /note= "Wild type amino acid substituted for Phe."

FT Misc-difference 21 /note= "Wild type amino acid substituted for Met."

FT Peptide 29..185

FT /label= Mature protein.

FT Misc-difference 30 /note= "Wild type amino acid substituted for Gly."

FT Misc-difference 43 /note= "Wild type amino acid substituted for Thr."

FT Misc-difference 150 /note= "Wild type amino acid substituted for Asn."

FT Misc-difference 171 /note= "Wild type amino acid substituted for Ala."

FT Misc-difference 197 /note= "Wild type amino acid substituted for Leu."

FT Misc-difference 203 /note= "Wild type amino acid substituted for Lys."

XX DE4226528-Al.

PN 17-FEB-1994.

XX 11-AUG-1992; 92DE-04226528.

XX 11-AUG-1992; 92DE-04226528.

XX (ROHG) ROEHM GMBH.

XX Gottschalk M, Sproesser B, Schuster E;

XX WPI; 1994-058089/08.

XX N-PSDB; AAQ56052.

XX New xylanase obtd. from Bacillus subtilis - useful in baking agents for
XX increased vol. of baking prods.

XX Claim 4; Page 10; lipp; German.

XX The modified xylanase is used as a baking agent, preferably for Yeast
XX pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 213 AA;

Query Match 96.5%; Score 1130; DB 2; Length 213;
Best Local Similarity 95.3%; Pred. No. 5, 6e-88;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MFKPKNLFVLGLSALMSISLFSATASAASTDYQWQNTDGGGVNNAVNGSGNGYVNVNSN 60

Db 1 MFKPKKFLVGLTAAFMSISMFSAATAGTDYQWQNTDGGGVNNAVNGSGNGYVNVNSN 60

Qy 61 TGNFVVGKWTGSPFRINYNAGVWAPNGCYLTYGWTSPLEIYYVVDWSWGTYPRTG 120

Db 61 TGNFVVGKWTGSPFRINYNAGVWAPNGCYLTYGWTSPLEIYYVVDWSWGTYPRTG 120

Qy 121 TYKGVTKSGGGTYDIYTTTRYNAPSIDGRTTFTQYWSVROSKRPTGSGNATITFSNHVNA 180

Db 121 TYKGVTKSGGGTYDIYTTTRYNAPSIDGRTTFTQYWSVROSKRPTGSGNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVATEGYQSSGSSNVTW 213

.

Db 181 WKSHGMNLGSNWAYQVATEGYKSSGSSNVTW 213

Search completed: February 3, 2006, 09:08:08
Job time : 201 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:04:53 ; Search time 246 Seconds
(without alignments)
610.884 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171

Sequence: 1 MFKPKNPLVGLSAAALMSIS.....YQVMATEGYQSSGSNTVTW 213

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	1 Xyna_BACSU	P18429 bacillus su
2	1168	99.7	213	1 Xyna_BACCI	P09850 bacillus ci
3	1166	99.6	213	2 Q59254 BACSU	Q59254 bacillus su
4	1165	99.5	213	2 Q59256 BACCI	Q59256 bacillus sp
5	1150	98.2	213	2 Q8RMN9 BACSU	Q8RMN9 bacillus su
6	1144	97.7	213	2 Q8RMN8 BACCI	Q8RMN8 bacillus ci
7	1127	96.2	213	2 Q92B36 BACSP	Q92B36 bacillus sp
8	1104	94.3	213	2 Q84F19 BACCI	Q84F19 bacillus sp
9	1096	93.6	213	2 Q8VVC3 BACCI	Q8VVC3 bacillus sp
10	945.5	80.7	212	2 Q9F9B9 BACCL	Q9F9B9 paenibacill
11	935.5	79.9	214	2 Q6TLP3 BACT	Q6TLP3 uncultured
12	930	79.4	210	1 Xyna_BACST	P45705 bacillus st
13	929	79.3	211	2 Q43993 AERPU	Q43993 aeromonas p
14	864.5	73.8	210	2 Q71S35 BACFI	Q71S35 bacillus fi
15	864.5	73.8	210	2 Q9KEF3 BACHD	Q9KEF3 bacillus ha
16	863.5	73.7	210	2 Q6U894 BACFI	Q6U894 bacillus fi
17	663.5	56.7	335	2 Q9RQB8 NMICO	Q9RQB8 xylanimicro
18	659	56.3	338	2 Q5Z265 THEFU	Q5Z265 thermomonos
19	659	56.3	338	2 Q8R298 THEFU	Q8R298 thermomonos
20	651.5	55.6	241	2 Q9RMH7 STROCO	Q9RMH7 streptomyc
21	646	55.2	329	2 Q9RMH9 STRVD	Q9RMH9 streptomyc
22	645.5	55.1	335	2 Q9RMH4 STRTM	Q9RMH4 streptomyc
23	639.5	54.6	335	2 Q76BV2 STRTL	Q76BV2 streptomyc
24	637	54.4	240	1 XINC STRLI	P26220 streptomyc
25	630	53.8	344	2 Q8GMV7 9ACTO	Q8GMV7 nonomuraea
26	626	53.5	191	2 Q9EM89 STROI	Q9EM89 streptomyc
27	622	53.1	228	2 Q59962 9ACTO	Q59962 streptomyc
28	621.5	53.1	228	2 Q4WG11 ASPFU	Q4WG11 aspergillus
29	621	53.0	240	2 Q56013 9ACTO	Q56013 streptomyc
30	610.5	52.1	417	2 Q693B5 9ALTE	Q693B5 microbulbif
31	609.5	52.0	644	1 XYND_CELFI	P54865 cellulomona

RESULT 1

ID	XYNA_BACSU	STANDARD;	PRT;	213 AA.
AC	P18429;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Endo-1,4-beta-xylanase A precursor (SC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan xylanohydrolase A).			
GN	Name=xyNA; OrderedLocusNames=BSU18840;			
OS	Bacillus subtilis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1423;			
[1]				
RP	NUCLEOTIDE SEQUENCE.			
RA	Paice M.G., Bourbonnais R., Desrochers M., Jurasek L., Yaguchi M.;			
RT	"A xylanase gene from Bacillus subtilis: nucleotide sequence and			
RT	comparison with B. pumilus gene.;"			
RL	Arch. Microbiol. 144:201-206(1986).			
[2]				
RP	NUCLEOTIDE SEQUENCE.			
RA	Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;			
RT	"Sequence analysis of the Bacillus subtilis chromosome region between			
RT	the terC and ohaB loci cloned in a yeast artificial chromosome.;"			
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
[3]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=168;			
PX	MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;			
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,			
RA	Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,			
RA	Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,			
RA	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,			
RA	Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,			
RA	Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,			
RA	Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,			
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,			
RA	Ghim S.-Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,			
RA	Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,			
RA	Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,			
RA	Jones L.-N., Joris B., Karamata D., Koningstein G., Krogh S.,			
RA	Klein C., Kobayashi Y., Koetter F., Koningstein G., Lauber J.,			
RA	Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Maue C.,			
RA	Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,			
RA	Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,			
RA	Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,			
RA	Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,			
RA	Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,			
RA	Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,			
RA	Scoffone F., Sekiguchi J., Sekowaka A., Seror S.J., Serror P.,			
RA	Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,			
RA	Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,			
RA	Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,			

ALIGNMENTS

ID	XYNA_BACSU	STANDARD;	PRT;	213 AA.
Q8VUT4	Q8VUT4_PSED			
P53332	emericella			
Q5B767	aspergillus			
P26515	streptomyce			
Q9KN6	streptomyce			
Q7ADQ1	neurospora			
Q81V5	chaetomium			
Q8G22	aspergillus			
Q6A21	aspergillus			
Q5AGR5	aspergillus			
P55330	aspergillus			
Q9HFA4	aspergillus			
P53333	emericella			
P48824	aspergillus			


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FT STRAND 43 48
FT TURN 51 52
FT STRAND 53 59
FT STRAND 63 70
FT TURN 75 76
FT STRAND 78 89
FT STRAND 92 101
FT TURN 102 104
FT STRAND 105 113
FT STRAND 121 128
FT TURN 129 130
FT STRAND 131 140
FT TURN 146 147
FT STRAND 150 160
FT STRAND 170 173
FT TURN 174 183
FT TURN 184 185
FT STRAND 191 202
FT STRAND 205 213
SQ SEQUENCE 213 AA; 23359 MW; 4BA0A35238CC0135 CRC64;

Query Match 99.7%; Score 1168; DB 1; Length 213;
Best Local Similarity 99.5%; Pred. No. 4e-86;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFKPKNFVLGLSAAALMSISLFSATASAASTDYWNQWTDGGGINVNAVNGSGGNYVNVNSN 60
DB 1 MFKPKNFVLGLSAAALMSISLFSATASAASTDYWNQWTDGGGINVNAVNGSGGNYVNVNSN 60

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEYYVVDWSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEYYVVDWSWGTYPRTG 120

QY 121 TYKGVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFNSHNVA 180
DB 121 TYKGVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFNSHNVA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 3
Q59254_BACSU PRELIMINARY; PRT; 213 AA.
AC Q59254;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Xylanase (EC 3.2.1.8).
GN Name=xvNA;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92140374; PubMed=1310524;
RA Niersbach M., Kreuzaler F., Geerse R.H., Postma P.W., Hirsch H.J.;
RT "Cloning and nucleotide sequence of the Escherichia coli K-12 ppsA
gene, encoding PEP synthase.";
RL Mol. Gen. Genet. 231:332-336(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168 ttpC2;
RX MEDLINE=95219081; PubMed=7704256;
RA Wolf M., Geczi A., Simon O., Borriess R.;
RT "Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus
subtilis: characterization, mapping and construction of strains
RT deficient in lichenase, cellulase and xylanase.";
RL Microbiology 141:281-290(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
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RC STRAIN=168 ttpC2;
RA Borriess R., Wolf M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z34519; CAA84276.1; -, Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q59254; 27-213.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 213 AA; 23355 MW; 21D76D4F8CED4B7 CRC64;

Query Match 99.6%; Score 1166; DB 2; Length 213;
Best Local Similarity 99.5%; Pred. No. 5.8e-86;
Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFKPKNFVLGLSAAALMSISLFSATASAASTDYWNQWTDGGGINVNAVNGSGGNYVNVNSN 60
DB 1 MFKPKNFVLGLSAAALMSISLFSATASAASTDYWNQWTDGGGINVNAVNGSGGNYVNVNSN 60

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEYYVVDWSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEYYVVDWSWGTYPRTG 120

QY 121 TYKGVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFNSHNVA 180
DB 121 TYKGVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFNSHNVA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 4
Q59256_9BACI PRELIMINARY; PRT; 213 AA.
AC Q59256;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Endo-1, 4-beta-xylanase precursor (EC 3.2.1.8).
GN Name=xvNS;
OS Bacillus sp. YA-14.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=72411;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YA-14;
RA Yu J.H., Park Y.S., Yum D.Y., Kim J.M., Kong I.S., Bai D.H.;
RT "Nucleotide sequence and analysis of a xylanase gene (xvns) from
alkali-tolerant Bacillus sp. YA-14 and comparison with other
xylanases.";
RL J. Microbiol. Biotechnol. 3:139-145(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YA-14;
RA Hyun Ju Y.;
RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; X59058; CAA41783.1; -, Genomic_DNA.
DR PIR; S48126; S48126.
DR HSSP; P09850; 1XNB.
DR SMR; Q59256; 27-213.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR
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DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 213 endo-1, 4-beta-xylanase.
SQ SEQUENCE 213 AA; 23341 MW; 2110D35768CC0034 CRC64;

Query Match 99.5%; Score 1165; DB 2; Length 213;
Best Local Similarity 99.1%; Pred. No. 7e-86;
Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVAVNGSGGNYVAVNSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVAVNGSGGNYVAVNSN 60

Qy 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLYTGYWTRSPLEIYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLYTGYWTRSPLEIYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQKPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 5
Q8RMN9_BACSU PRELIMINARY; PRT; 213 AA.
AC Q8RMN9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1, 4-xylanase.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN NUCLEOTIDE SEQUENCE.
RA Sun J., Gu S., Li W., Xiao H., Xiao J., Fu L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490979; AAM08359.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8RMN9; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23277 MW; 34DFAD4D9C2C0034 CRC64;

Query Match 98.2%; Score 1150; DB 2; Length 213;
Best Local Similarity 98.6%; Pred. No. 1.1e-84;
Matches 210; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVAVNGSGGNYVAVNSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVAVNGSGGNYVAVNSN 60

Qy 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLYTGYWTRSPLEIYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLYTGYWTRSPLEIYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQKPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 6
Q8RMN8_BACCI PRELIMINARY; PRT; 213 AA.
AC Q8RMN8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1, 4-xylanase.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN NUCLEOTIDE SEQUENCE.
RA Sun J., Xu Z., Li W., Gu S., Zhao H., Xiao J., Chen Y.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490980; AAM08360.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8RMN8; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23378 MW; E306B98D49E8CF4D CRC64;

Query Match 97.7%; Score 1144; DB 2; Length 213;
Best Local Similarity 97.7%; Pred. No. 3.4e-84;
Matches 208; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVAVNGSGGNYVAVNSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVAVNGSGGNYVAVNSN 60

Qy 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLYTGYWTRSPLEIYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRITINAGVWAPNGNGYLYTGYWTRSPLEIYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQKPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 7
Q9ZB36_BACSP PRELIMINARY; PRT; 213 AA.
AC Q9ZB36;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1, 4-beta-xylanhydrolase.
GN Name=xyna;
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN NUCLEOTIDE SEQUENCE.
RA Kim S.C., Jeong K.J., Kim M.S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U51675; AAD10834.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q9ZB36; 27-213.

DR	GO: 0016787; F:hydrolase activity; IEA.
DR	GO: 0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR	GO: 0005975; P:carbohydrate metabolism; IEA.
DR	InterPro: IPR001137; Glyco hydro_11.
DR	Pfam: PF00457; Glyco hydro_11; 1.
DR	PRINTS; PR00911; GLHYDLASE11.
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW	Hydrolase.
SEQ	SEQUENCE 213 AA; 23277 MW; 3A1DEE1139E3358B CRC64;
	Query Match 96.2%; Score 1127; DB 2; Length 213;
	Best Local Similarity 94.8%; Pred. No. 8e-83; Indels 0; Gaps 0;
	Matches 202; Conservative 5; Mismatches 6;
Qy	1 MFKEFKQFLVGLSAAALMSISLFSATASAASTDYQNWTTDGGGVNANVNGSGGNTSVNWSN 60
Db	1 MFKEFKKFLVGLTAFAFMSISFESATASAAGTDYQNWTTDGGGVNANVNGSGGNTSVNWSN 60
Qy	61 TGNFVVGKWTGSPFRTINTNAGWAPNGNGYTLYGWTRSPLEIYYVVDVSWGYRPTG 120
Db	61 TGNFVVGKWTGSPFRTINTNAGWAPNGNGYTLYGWTRAPLEIYYVVDVSWGYRPTG 120
Qy	121 TYKGTVKSDDGYTDIYTYTRYNAPSIDGDRITFTQYNSVRSKPTGTSNATITFSNHVA 180
Db	121 TYKGTVKSDDGYTDIYTYTRYNAPSIDGDNITFTQYNSVRSKPTGTSNAAITFSNHVA 180
Qy	181 WKSHGMNLGSNWAYQVMATEGYQSGSGSNVTVM 213
Db	181 WKSHGMNLGSNWAYQVLTAGEYKSGSGSNVTVM 213
RESULT 8	
ID	Q84F19_9BAC1
ID	Q84F19_9BAC1 PRELIMINARY; PRT; 213 AA.
AC	Q84F19;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Endo-1,4-beta-xylanase A precursor.
GN	Name=xYnA;
OS	Bacillus sp. BP-7.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX	NCBI_TaxID=126733;
ON	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	PubMed=15057452; DOI=10.1007/s00284-003-4196-0;
RA	Gallardo O., Diaz P., Pastor F.I.J.;
RT	"Cloning and characterization of xylanase A from the strain Bacillus
RT	sp. BP-7: comparison with alkaline pi-low molecular weight xylanases
RT	of family 11.";
RL	Curr. Microbiol. 48:276-279 (2004).
DR	EMBL; AJ536759; CAD60654.1; -; Genomic_DNA.
DR	HSSP; P09850; 1XNB.
DR	SMR; Q84F19; 27-213.
DR	GO: 0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR	GO: 0005975; P:carbohydrate metabolism; IEA.
DR	GO: 0045493; P:xylan catabolism; IEA.
DR	InterPro: IPR001137; Glyco_hydro_11.
DR	Pfam; PF00457; Glyco_hydro_11; 1.
DR	PRINTS; PR00911; GLHYDLASE11.
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW	Signal; Xylan degradation.
FT	SIGNAL 1 28 Potential.
FT	CHAIN 29 213 endo-1,4-beta-xylanase A.
SEQ	SEQUENCE 213 AA; 23475 MW; F1E194D24A329516 CRC64;
	Query Match 94.3%; Score 1104; DB 2; Length 213;
	Best Local Similarity 93.0%; Pred. No. 5.7e-81;
	Matches 198; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
Qy	1 MFKEFKQFLVGLSAAALMSISLFSATASAASTDYQNWTTDGGGVNANVNGSGGNTSVNWSN 60

Db 1 MFKEFKRFLVGLTFAALMSISLFSANAGASANTDYQWNTDGGGTVNAVNGSGGNYSVNWSN 60

Qy 61 TGNFVVGKGMTTGGSPFRRTINYNAGVWAPNGNGYLTLTGWTRSPLEIYYVVDVSWGTYRPTG 120
 |||||
 Db 61 TGNFVVGKGMTTGGSPFRRTINYNAGVWAPNGNAYLTLTGWRSPLEIYYVVDVSWGTYRPTG 120
 |||||

Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKPTGNSNAITITSNHVA 180
 |||||
 Db 121 TYKGTVKSDDGTYDVYTTTRYDAPSIDGDKTFTQYWSVRQSKPTGNSNAITITSNHVA 180
 |||||

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
 |||.|||||
 Db 181 WKRYGMNLGSNWSYQVLATEGYQSSGSSNVTVM 213
 |||.|||||

RESULT 9

Q8VVC3_9BACI PRELIMINARY; PRT; 213 AA.

AC Q8VVC3;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Endo-xylanase.

GN Name=xyl1;

OS *Bacillus* sp. NBL420.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

OX NCBI_TaxID=165829;

EN [1]

RP NUCLEOTIDE SEQUENCE.

RA Hong I.P., Lee S.Y., Choi S.G.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF441773; AAL32473.1; -; Genomic_DNA.

DR HSSP; P09850; 1XNB.

DR SMR; Q8VVC3; 27-213.

DR GO; GO:000453; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR GO; GO:0045493; P:xylan catabolism; IEA.

DR InterPro; IPR001137; Glyco_hydro_11.

DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GLHYDRASE11.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_Fil_1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_Fil_2; 1.

KW xylan degradation.

SQ SEQUENCE 213 AA; 23341 MW; 4CCODFF5E525E7551 CRC64;

Query March 93.6%; Score 1096; DB 2; Length 213;
 Best Local Similarity 92.5%; Pred. No. 2.5e-80;
 Matches 197; Conservative 8; Mismatches 8; Indels 0; Gaps 0

Qy 1 MFKEFKRFLVGLSAAALMSISLFSATAAASDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
 |||||
 Db 1 MFKEFKRFLVGLTFAALMSISLFSATAAASPDYQWNTDGGGTVNAVNGPGGNYSVNWSN 60
 |||||

Qy 61 TGNFVVGKGMTTGGSPFRRTINYNAGVWAPNGNGYLTLTGWTRSPLEIYYVVDVSWGTYRPTG 120
 |||||
 Db 61 TGNFVVGKGMTTGGSPRTINYNAGVWAPNGNGYLALYGTWTRAPLEIYYVVDVSWGTYRPTG 120
 |||||

Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKPTGNSNAITITSNHVA 180
 |||||
 Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDKTFTQYWSVRQSKPTGNSNAITITSNHVA 180
 |||||

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
 |||||
 Db 181 WKSHGMNLGSNWSYQVLATEGYQSSGSSNVTVM 213
 |||||

RESULT 10

Q9F9B9_9BACI PRELIMINARY; PRT; 212 AA.

AC Q9F9B9;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2004 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

RESIT.T 10

Q9F9B9_9BACL	
ID	Q9F9B9_9BACL PRELIMINARY; PRT; 212 AA.
AC	Q9F9B9;
DT	01-MAR-2001 (TREMBlrel. 16, Created)
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DR		PROSITE; PS00776;	GLYCOSYL_HYDROL_Fll_1;	UNKNOWN 1.
DR		PROSITE; PS00777;	GLYCOSYL_HYDROL_Fil_2;	1.
KW	Glycosidase,	Hydrolase; Signal;	Xylan degradation.	
FT	SIGNAL	1	Potential.	
SQ	SEQUENCE	214 AA;	23478 MW; 6FDICB9BB6GA5048 CRC64;	
	Query Match	79.9%;	Score 935.5;	DB 2; Length 214;
	Best Local Similarity	80.4%;	Pred No.2.le-67;	
Matches	I72; Conservative	13;	Mismatches 28;	Indels 1; Gaps 1;
Qy	1	MPKFKCNFLVLGSAALMS-ISLFSATASAASTDYWQNWDGGGI VNAVNGSGGNYSVNSWS	59	
Dq	1	MFPKLSKKILMVLITISMSFSLFTVTAYAASTDYWQNWDGGGT VNATNGSDGNGSVSWS	60	
Qy	60	NTCNFVVVGKWTTGSPPRINTYNAGWPANGNYLTLYGWTSRLPIEYYVDSWGTVRP	119	
Dq	61	NCNCFVVVGKWTTGSTATRNVINAGAFSPSGNGIYLALYGWRNSLI EYYVDSWGTYRPT	120	
Qy	120	GTKYGVTKSDGGGYDIYTTRTNAPSIDGDRTTFTQYWSVRQSRRP TGSNAITTFSNHVN	179	
Dq	121	GTKYGVTKSDGGGYDYITTRTNAPSIDGNNTTFTQFW SVRSQRPIGTNNITTFFSNHN	180	
Qy	180	AKWSHGMNLGSNWAOYMATEGYQSSGSSNVIVW	213	
Dq	181	AWKSCKMNLGSSWSYOVLATEGYQSSGYSNVIVW	214	
RESULT 12				
XYNA_BACST				
ID_XYNA_BACST	STANDARD;	FRT;	210 AA.	
AC_P45705;				
DT_01-NOV-1995	(Rel. 32, Created)			
DT_15-JUL-1998	(Rel. 36, Last sequence update)			
DT_10-MAY-2005	(Rel. 47, Last annotation update)			
DE_Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A) (1,4-				
DE_beta-D-xylan xylanohydrolase A).				
DN_Name=xyNA;				
GN Bacillus stearothermophilus.				
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.				
OX NCBI_TaxId=1422;				
RN [1]				
RP NUCLEOTIDE SEQUENCE.				

```

RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from
RT Bacillus stearothermophilus.";
RT J. Microbiol. Biotechnol. 5:117-124 (1995).
RN [2]
RN
RN SEQUENCE REVISION.
RN
RA Cho S., Choi Y.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RC
RC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
RC linkages in xylans.
CC
CC -1- PATHWAY: Xylan degradation.
CC
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC
CC EMBL; U15985; AAB72117.1; -; Genomic_DNA.
CC HSSP; P09850; 1XNB.
CC SRR; P457085; 24-210.
CC InterPro; IPR001137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHYDRASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F12_1; 1.
CC Glycosidase; Hydrolase; Signal; Xylan degradation.
CC SIGNAL 1 19 potential.
CC FT

```

FT CHAIN 20 210 Endo-1,4-beta-xylanase A.
 FT ACT SITE 104 104 Nucleophile (By similarity).
 FT ACT SITE 197 197 Proton donor (By similarity).
 SQ SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 79.4%; Score 930; DB 1; Length 210;
 Best Local Similarity 80.6%; Pred. No. 5.6e-67;
 Matches 170; Conservative 11; Mismatches 28; Indels 2; Gaps 2;

QY 3 KFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGGNYSVNWSNTG 62
 Db 2 KKKKWLTLTLLTASNSFGLFGATSSAA-TDYQWNTDGGGMVNAVNGPGNYSVTMQNTG 60

QY 63 NFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVSWGTYRPTGY 122
 Db 61 NFVVGKWTGSPNRYINYNAGVWAPNGNGYLTLGWTRNALLIYYVVDVSWGTYRPTGNY 120

QY 123 KGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNAWK 182
 Db 121 KGTVNSDDGTYDIYTTTRYNAPSIDGTO-TFQFWSVRQSKRPTGNSNATITFSNVHNAWR 179

QY 183 SHGMNLGSSWAYQVMATEGYQSSGSSNVTW 213
 Db 180 SKGMNLGSSWAYQVLAATEGYQSSGSSNVTW 210

RESULT 13
 Q43993_AERPU PRELIMINARY; PRT; 211 AA.
 AC Q43993;
 DT 01-NOV-1996 (TremBLrel. 01, Created)
 DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
 DE Xylanase I precursor.
 GN Name-xyna;
 OS Aeromonas punctata (Aeromonas caviae).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OX NCBI_TaxID=648;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ME-1; TISSUE=Gut content of silk worm;
 RA Kubata K.B., Suzuki T., Horitsu H., Kawai K., Takamizawa K.;
 RT "Xylanase I of Aeromonas caviae ME-1 isolated from the intestine of a
 RT herbivorous insect (Samia cynthia pyralis).";
 RL Biosci. Biotechnol. Biochem. 56:1463-1464(1992).
 RN [2]

QY 1) of Aeromonas caviae ME-1;
 RT Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RL EMBL; D32065; BAA06837.1; -; Genomic_DNA.
 DR HSSP; P09850; 1XNB.
 DR SMR; Q43993; 25-211.
 DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0045493; P:xylan catabolism; IEA.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Signal; Xylan degradation.
 FT SIGNAL 1 28 Potential.
 FT CHAIN 29 211 xylanase I.
 SQ SEQUENCE 211 AA; 23136 MW; F9E30403EB935E49 CRC64;

* Query Match 79.3%; Score 929; DB 2; Length 211;
 Best Local Similarity 79.3%; Pred. No. 6.8e-67;
 Matches 169; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

QY 1 MFKFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGGNYSVNWSN 60
 Db 1 MFKFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGGNYSVNWSN 59

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVSWGTYRPTG 120
 Db 60 TGNFVVGKWTGSPNRYINYNAGVWAPNGNGYLTLGWTRNALLIYYVVDVSWGTYRPTG 119

QY 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNA 180
 Db 120 TYKGTVNSDDGTYDIYTTTRYNAPSIDGTO-TFQFWSVRQSKRPTGNSNATITFSNVHNA 178

QY 181 WSHGMNLGSSWAYQVMATEGYQSSGSSNVTW 213
 Db 179 WPSKGMNLGSSWAYQVLAATEGYQSSGSSNVTW 211

RESULT 14
 Q71S35_BACFI PRELIMINARY; PRT; 210 AA.
 AC Q71S35;
 DT 05-JUL-2004 (TremBLrel. 27, Created)
 DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
 DE Xylanase.
 OS Bacillus firmus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1399;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-1;
 RA Chuensumran U., Ratanakhanokchai K., Cheevadhanarak S.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF317173; AAQ14588.1; -; Genomic_DNA.
 DR HSSP; P09850; 1BCX.
 DR SMR; Q71S35; 27-210.
 DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0045493; P:xylan catabolism; IEA.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYDRLASE1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation.
 SQ SEQUENCE 210 AA; 23313 MW; AC4BA5DD5D67A1B2 CRC64;

Query Match 73.8%; Score 864.5; DB 2; Length 210;
 Best Local Similarity 74.2%; Pred. No. 1.1e-61;
 Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 1 MFKFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGGNYSVNWSN 60
 Db 1 MFKFKKFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYVNAVNGSGGNYSVNWSN 58

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVSWGTYRPTG 120
 Db 59 TGNFVVGKWTGSPNRYINYNAGVWAPNGNGYLTLGWTRNALLIYYVVDVSWGTYRPTG 118

QY 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGNSNATITFSNVHNA 180
 Db 119 THRGTVNSDDGTYDIYTTTRYNAPSIDGTO-TFQFWSVRQSKRPTGNSNATITFSNVHNA 177

QY 181 WSHGMNLGSSWAYQVMATEGYQSSGSSNVTW 213
 Db 178 WRNAGMNLGSSWAYQVLAATEGYQSSGSSNVTW 210

RESULT 15
 Q9KEF3_BACHD PRELIMINARY; PRT; 210 AA.
 AC Q9KEF3;
 DT 01-OCT-2000 (TremBLrel. 15, Created)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2006, 09:11:33 ; Search time 28 Seconds
(without alignments)
628.926 Million cell updates/sec

Title: US-10-626-724-5
Perfect score: 1171
Sequence: 1 MFKFKNPLVGLSALMSIS.....YQVMATEGYQSSGSNTVTW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/pCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.7	213	2	US-09-570-856B-1
2	1168	99.7	213	2	US-09-570-856B-13
3	1141	97.4	208	1	US-08-315-695-21
4	1130	96.5	213	1	US-08-104-445-3
5	1041	88.9	185	1	US-08-044-621D-37
6	1041	88.9	185	1	US-08-709-912-5
7	1041	88.9	185	1	US-09-047-370-5
8	1038	88.6	185	1	US-08-044-621D-36
9	1038	88.6	185	1	US-08-709-912-3
10	1038	88.6	185	1	US-09-047-370-3
11	987	84.3	185	2	US-09-570-856B-5
12	987	84.3	185	2	US-09-570-856B-9
13	979	83.6	185	2	US-09-570-856B-7
14	977	83.4	185	2	US-09-570-856B-4
15	976	83.3	185	2	US-09-570-856B-6
16	974	83.2	185	2	US-09-570-856B-3
17	955	81.6	185	2	US-09-570-856B-10
18	955	81.6	211	1	US-08-575-964-1
19	955	81.6	211	1	US-08-963-500-1
20	951	81.2	185	2	US-09-570-856B-12
21	933	79.7	185	2	US-09-570-856B-8
22	920	78.6	185	2	US-09-570-856B-11
23	640.5	54.7	189	1	US-08-709-912-13
24	640.5	54.7	189	1	US-09-047-370-13
25	637	54.4	240	2	US-09-570-856B-16
26	636	54.3	344	1	US-08-468-812-2
27	636	54.3	344	2	US-08-590-563-2

28	636	54.3	344	2	US-09-770-621-2	Sequence 2, Appli
29	636	54.3	344	2	US-09-235-832-2	Sequence 2, Appli
30	635	54.2	216	1	US-08-315-695-20	Sequence 20, Appli
31	627.5	53.6	200	1	US-07-744-570B-2	Sequence 2, Appli
32	625.5	53.4	191	1	US-08-044-621D-35	Sequence 35, Appli
33	618.5	52.8	191	1	US-08-709-912-11	Sequence 11, Appli
34	618.5	52.8	191	1	US-09-047-370-11	Sequence 11, Appli
35	594	50.7	206	1	US-08-315-695-19	Sequence 19, Appli
36	594	50.7	215	1	US-08-044-621D-34	Sequence 34, Appli
37	594	50.7	335	2	US-09-570-856B-15	Sequence 15, Appli
38	587	50.1	191	1	US-08-709-912-10	Sequence 10, Appli
39	587	50.1	191	1	US-09-047-370-10	Sequence 10, Appli
40	585.5	50.0	230	2	US-08-768-373-4	Sequence 4, Appli
41	585.5	50.0	230	2	US-08-849-242A-4	Sequence 4, Appli
42	583.5	49.8	225	1	US-08-290-979A-8	Sequence 8, Appli
43	579	49.4	189	1	US-08-044-621D-33	Sequence 33, Appli
44	573.5	49.0	225	2	US-09-570-856B-26	Sequence 26, Appli
45	572	48.8	189	1	US-08-709-912-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-570-856B-1
; Sequence 1, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Basil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570.856B
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus circulans
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(28)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (29)..()
; OTHER INFORMATION:
US-09-570-856B-1

Query Match 99.7%; Score 1168; DB 2; Length 213;
Best Local Similarity 99.5%; Pred. No. 6.3e-98;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGIYVAVNGSGNYSVWNSN 60
Db 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGIYVAVNGSGNYSVWNSN 60
QY 61 TGNFVVGKWTGTPPRTINTNAGVAPNGNGYLYLWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGTPPRTINTNAGVAPNGNGYLYLWTRSPLEIYYVVDVSWGTYRPTG 120
QY 121 TYKGTVKSDDGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFTHVNA 180
Db 121 TYKGTVKSDDGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFTHVNA 180
QY 181 WKSHGMNLGSNWAVQVMATEGYQSSGSNTVTW 213
Db 181 WKSHGMNLGSNWAVQVMATEGYQSSGSNTVTW 213

RESULT 2

US-09-570-856B-13

; Sequence 13, Application US/09570856B

; Patent No. 6682923

; GENERAL INFORMATION:

; APPLICANT: Bentzien, Joerg M

; APPLICANT: Dahiyat, Bassil I

; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE

; FILE REFERENCE: A-67478-1/RFT/RMS/RMK

; CURRENT APPLICATION NUMBER: US/09/570,856B

; CURRENT FILING DATE: 2002-04-15

; PRIOR APPLICATION NUMBER: US 60/133,714

; PRIOR FILING DATE: 1999-05-12

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Bacillus subtilis

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)..(28)

; OTHER INFORMATION:

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: (29)..()

; OTHER INFORMATION:

; US-09-570-856B-13

Query Match

Best Local Similarity 99.7%; Score 1168; DB 2; Length 213;

Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFKFKNPLVGLSAAALMSISLFSATASASTDYQWQNTDGGGINAVNGSGGNTSVNWSN	60
Db	1	MFKFKNPLVGLSAAALMSISLFSATASASTDYQWQNTDGGGINAVNGSGGNTSVNWSN	60
Qy	61	TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG	120
Db	61	TGNFVVGKWTGSPFRITINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG	120
Qy	121	TYKGTVKSDBGTYDIYITRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA	180
Db	121	TYKGTVKSDBGTYDIYITRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA	180
Qy	181	WKSNGMLGSNWAYQVMATEGYQSSGSSNVTVW	213
Db	181	WKSNGMLGSNWAYQVMATEGYQSSGSSNVTVW	213

RESULT 3

US-08-315-695-21

; Sequence 21, Application US/08315695

; Patent No. 5591619

; GENERAL INFORMATION:

; APPLICANT: Li, Xin-Liang

; APPLICANT: Ljungdahl, Lars G.

; TITLE OF INVENTION: Aureobasidium Pullulans Xylanase, Gene

; TITLE OF INVENTION: and Signal Sequence

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Greenlee and Winner, P.C.

; CITY: Boulder

; STATE: CO

; COUNTRY: US

; ZIP: 80303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/315,695

; FILING DATE: 30-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winner, Ellen P.

; REGISTRATION NUMBER: 28,547

; REFERENCE/DOCKET NUMBER: 55-94

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 499-8080

; TELEFAX: (303) 499-8089

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 208 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; US-08-315-695-21

Query Match

Best Local Similarity 97.4%; Score 1141; DB 1; Length 208;

Matches 207; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	6	KNFLVGLSAAALMSISLFSATASASTDYQWQNTDGGGINAVNGSGGNTSVNWSNTGNFV	65
Db	1	KNFLVGLSAAALMSISLFSATASASTDYQWQNTDGGGINAVNGSGGNTSVNWSNTGNFV	60
Qy	66	VGKGTWTTGSPFRITINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGYKGT	125
Db	61	VGKGTWTTGSPFRITINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGYKGT	120
Qy	126	VKSDGGTYDIYITRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNAWKSHG	185
Db	121	VKSDGGTYDIYITRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFTNHVNAWKSHG	180
Qy	186	MNLGSNWAYQVMATEGYQSSGSSNVTVW	213
Db	181	MNLGSNWAYQVMATEGYQSSGSSNVTVW	208

RESULT 4

US-08-104-445-3

; Sequence 3, Application 08/104445

; Patent No. 5306633

; GENERAL INFORMATION:

; APPLICANT: GOTTSCHALK, MICHAEL

; APPLICANT: SCHUSTER, ERWIN

; APPLICANT: SPROESSLER, BRUNO

; TITLE OF INVENTION: BACTERIAL XYLANASE, METHOD FOR ITS

; TITLE OF INVENTION: PRODUCTION, BACTERIA PRODUCING A XYLANASE, DNA FRAGMENT

; TITLE OF INVENTION: ENCODING A XYLANASE, PLASMID CONTAINING THE DNA FRAGMENT,

; TITLE OF INVENTION: BAKING AGENTS CONTAINING A XYLANASE, AND METHOD FO

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: 08/104,445

; FILING DATE:

; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: ODION, No. 530663man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 583-179-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-445-3

Query Match 96.5%; Score 1130; DB 1; Length 213;
Best Local Similarity 95.3%; Pred. No. 1.7e-94;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFKPKKFLVGLSALMSISLFSATASAASTDYWNQWTDGGGIVNAVNGSGGNYSVNWSN 60
DB 1 MFKPKKFLVGLTAAFMSISLFSATASAASTDYWNQWTDGGGIVNAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRINYNAGVWAPNGNGLYLYGWTRSPLEIYYVVDVSWGTYRPTG 120
DB 61 TGNFVVGKWTGSPFRINYNAGVWAPNGNGLYLYGWTRSPLEIYYVVDVSWGTYRPTG 120

QY 121 TYKGVKSDGGTYDIYTTTRYNAPSIDGRTFTQYWSVROSKRPTGNSNATITFSNHVNA 180
DB 121 TYKGVKSDGGTYDIYTTTRYNAPSIDGRTFTQYWSVROSKRPTGNSNATITFSNHVNA 180

QY 181 WKSHGMNLSNWAYQVMTATEGYQSSGSSNVTVM 213
DB 181 WKSHGMNLSNWAYQVMTATEGYQSSGSSNVTVM 213

RESULT 5
US-08-044-621D-37
Sequence 37, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowing, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796

TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 185
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Bacillus subtilis
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Paice M.G., Bourbonnais R., Desrochers
AUTHORS: M., Jurasek L., & Yaguchi M.
TITLE:
JOURNAL: Arch. Microbiol.
VOLUME: 144
ISSUE:
PAGES: 201-206
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-37

Query Match 88.9%; Score 1041; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ASTDYWNQWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTINYNAGVWAP 88
DB 1 ASTDYWNQWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTINYNAGVWAP 60

QY 89 NNGYLYLYGWTRSPLEIYYVVDVSWGTYRPTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
DB 61 NNGYLYLYGWTRSPLEIYYVVDVSWGTYRPTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120

QY 149 DRTTFTQYWSVROSKRPTGNSNATITFSNHVNAWKSHGMNLSNWAYQVMTATEGYQSSGSS 208
DB 121 DRTTFTQYWSVROSKRPTGNSNATITFSNHVNAWKSHGMNLSNWAYQVMTATEGYQSSGSS 180

QY 209 NVTVM 213
DB 181 NVTVM 185

RESULT 6
US-08-709-912-5
Sequence 5, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORGANISM: Bacillus subtilis
PUBLICATION INFORMATION:
AUTHORS: Parce, M.G.
AUTHORS: Bourbonnais, R
AUTHORS: Desrochers, M
AUTHORS: Jurasek, L
AUTHORS: Yaguchi, M
JOURNAL: Arch. Microbiol.
VOLUME: 144
PAGES: 201-206
DATE: 1986
US-08-709-912-5

Query Match 88.9%; Score 1041; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 29 ASTDYQNWTDGGGINVAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTINYNAGVWAP 88
Db 1 ASTDYQNWTDGGGINVAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTINYNAGVWAP 60
Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120
Qy 149 DRTFTQYWSVRQSKRPTGSGNATITFSNHNAMKSHGMLGNSWAYQVMATEGYQSSGSS 208
Db 121 DRTFTQYWSVRQSKRPTGSGNATITFSNHNAMKSHGMLGNSWAYQVMATEGYQSSGSS 180
Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 7
US-09-047-370-5
Sequence 5, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
Thermophilicity, Alkalophilicity and

TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Bacillus subtilis
PUBLICATION INFORMATION:
AUTHORS: Parce, M.G.
AUTHORS: Bourbonnais, R
AUTHORS: Desrochers, M
AUTHORS: Jurasek, L
AUTHORS: Yaguchi, M
JOURNAL: Arch. Microbiol.
VOLUME: 144
PAGES: 201-206
DATE: 1986
US-09-047-370-5

Query Match 88.9%; Score 1041; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 29 ASTDYQNWTDGGGINVAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTINYNAGVWAP 88
Db 1 ASTDYQNWTDGGGINVAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTINYNAGVWAP 60
Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120
Qy 149 DRTFTQYWSVRQSKRPTGSGNATITFSNHNAMKSHGMLGNSWAYQVMATEGYQSSGSS 208
Db 121 DRTFTQYWSVRQSKRPTGSGNATITFSNHNAMKSHGMLGNSWAYQVMATEGYQSSGSS 180
Qy 209 NVTVM 213
Db 181 NVTVM 185


```
Db 181 NVTW 185

RESULT 12
US-09-570-856B-9
; Sequence 9, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-9

Query Match 84.0%; Score 984; DB 2; Length 185;
Best Local Similarity 93.5%; Pred. No. 2.3e-81;
Matches 173; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGWAP 60

Qy 89 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 14
US-09-570-856B-4
; Sequence 4, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 185
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-4

Query Match 83.4%; Score 977; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 9.8e-81;
Matches 174; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGWAP 60

Qy 89 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGVLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTW 213
Db 181 NVTW 185

RESULT 15
US-09-570-856B-6
; Sequence 6, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 185
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-6

Query Match 83.6%; Score 979; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 6.5e-81;
Matches 174; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:12:33 ; Search time 8 Seconds
(without alignments)
311.993 Million cell updates/sec

Title: US-10-626-724-5

Perfect score: 1171

Sequence: 1 MFKEFKNFLVGLSAAALMSIS.....YQNMATEGYQSGSSNTVTW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.New.*

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	100.0	213	6	US-10-517-939-188
2	1171	100.0	213	7	US-11-170-653-16
3	1168	99.7	213	6	US-10-517-939-224
4	1168	99.7	213	7	US-11-170-653-17
5	1104	94.3	213	6	US-10-517-939-230
6	1097	93.7	213	6	US-10-517-939-302
7	1041	88.9	185	7	US-11-170-653-1
8	953	81.4	211	6	US-10-517-939-198
9	933.5	79.7	214	6	US-10-517-939-158
10	929	79.3	211	7	US-11-170-653-19
11	927	79.2	210	6	US-10-517-939-208
12	907.5	77.5	211	7	US-11-170-653-18
13	886	75.7	189	6	US-10-517-939-190
14	873.5	74.6	184	6	US-10-517-939-252
15	844	72.1	189	6	US-10-517-939-380
16	834	71.2	189	6	US-10-517-939-378
17	826	70.5	189	6	US-10-517-939-376
18	710	60.6	222	6	US-10-517-939-168
19	687	58.7	445	6	US-10-517-939-368
20	669.5	57.2	225	6	US-10-517-939-172
21	663.5	56.7	241	7	US-11-170-653-43
22	659	56.3	240	7	US-11-170-653-42
23	658	56.2	361	6	US-10-517-939-212
24	647.5	55.3	355	6	US-10-517-939-206
25	646	55.2	242	7	US-11-170-653-41

ALIGNMENTS

RESULT 1

US-10-517-939-188
; Sequence 188, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-188

Query Match 100.0%; Score 1171; DB 6; Length 213;

Best Local Similarity 100.0%; Pred. No. 7.6e-96;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFKEFKNFLVGLSAAALMSISLFSATASATDYQNNTDGGIYNVNGSGNTSVNWSN	60
Db	1	MFKEFKNFLVGLSAAALMSISLFSATASATDYQNNTDGGIYNVNGSGNTSVNWSN	60
Qy	61	TGNFVVGKGMTTGPFRFTINYNAGVWAPNGNYLTLYGWTSPLEIYYVVDVSWGTYRPTG	120
Db	61	TGNFVVGKGMTTGPFRFTINYNAGVWAPNGNYLTLYGWTSPLEIYYVVDVSWGTYRPTG	120
Qy	121	TYKGTVSKDGGTYDIYTRYNAPSIDGDRTPFTQYVSVROSKEPTGSAITTSNHNVA	180

Db 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 2

US-11-170-653-16

; Sequence 16, Application US/11170653

; Publication No. US20050271769A1

; GENERAL INFORMATION:

; APPLICANT: Danisco A/S

; APPLICANT: Sibbesen, Ole

; APPLICANT: Sorensen, Jens

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

; FILE REFERENCE: 674509-2046

; CURRENT APPLICATION NUMBER: US/11/170,653

; CURRENT FILING DATE: 2005-06-23

; PRIOR APPLICATION NUMBER: US/10/237,386

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: PCT/IB01/00426

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: GB 0005585.5

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 16

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Bacillus subtilis

US-11-170-653-16

Query Match 100.0%; Score 1171; DB 7; Length 213;

Best Local Similarity 100.0%; Pred. No. 7.6e-96;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKKQFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60

Db 1 MFKFKKQFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Qy 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Db 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 3

US-10-517-939-224

; Sequence 224, Application US/10517939

; Publication No. US20060003433A1

; GENERAL INFORMATION:

; APPLICANT: Steer, Brian

; APPLICANT: Callen, Walter

; APPLICANT: Healey, Shaun

; APPLICANT: Hazlewood, Geoff

; APPLICANT: Wu, Di

; APPLICANT: Blum, David

; APPLICANT: Esseglihan, Alireza

; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

; FILE REFERENCE: 564462007901

; CURRENT APPLICATION NUMBER: US/10/517,939

; CURRENT FILING DATE: 2004-12-13

Qy 1 MFKFKKQFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60

Db 1 MFKFKKQFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Qy 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Db 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 4

US-11-170-653-17

; Sequence 17, Application US/11170653

; Publication No. US20050271769A1

; GENERAL INFORMATION:

; APPLICANT: Danisco A/S

; APPLICANT: Sibbesen, Ole

; APPLICANT: Sorensen, Jens

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

; FILE REFERENCE: 674509-2046

; CURRENT APPLICATION NUMBER: US/11/170,653

; CURRENT FILING DATE: 2005-06-23

; PRIOR APPLICATION NUMBER: US/10/237,386

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: PCT/IB01/00426

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: GB 0005585.5

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 17

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Bacillus circulans

US-11-170-653-17

Query Match 99.7%; Score 1168; DB 7; Length 213;

Best Local Similarity 99.5%; Pred. No. 1.4e-95;

Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKKQFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60

Db 1 MFKFKKQFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDWSWGTYRPTG 120

Qy 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Db 121 TYKGTAKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGNSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLTLGWTSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLTLGWTSPLEIYYVVDVDSWGTYPRTG 120
Qy 121 TYKGTVKSDDGTYDYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 5

US-10-517-939-230
; Sequence 230, Application US/10517939
; Publication No. US20060003433A1

GENERAL INFORMATION:

; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample

; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-230
Query Match 94.3%; Score 1104; DB 6; Length 213;
Best Local Similarity 93.0%; Pred. No. 5.5e-90;
Matches 198; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
Qy 1 MFKEKKNFLVGLSALMSISLFSATASASTDYQWNTDGGIYNVANGSGNYSVNWNSN 60
Db 1 MFKEKKNFLVGLTAAALMSLSLFSANASANTDYQWNTDGGIYNVANGSGNYSVNWNSN 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLTLGWTSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLTLGWTSPLEIYYVVDVDSWGTYPRTG 120
Qy 121 TYKGTVKSDDGTYDYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKRYGMNLGSNWYQVLATEGYQSSGSSNVTW 213

RESULT 6

US-10-517-939-302
; Sequence 302, Application US/10517939
; Publication No. US20060003433A1

GENERAL INFORMATION:

; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-302

Query Match 93.7%; Score 1097; DB 6; Length 213;
Best Local Similarity 92.0%; Pred. No. 2.3e-89;
Matches 196; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSALMSISLFSATASASTDYQWNTDGGIYNVANGSGNYSVNWNSN 60
Db 1 MFKEKKNFLVGLTAAALMSLSLFSANASANTDYQWNTDGGIYNVANGSGNYSVNWNSN 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLTLGWTSPLEIYYVVDVDSWGTYPRTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLTLGWTSPLEIYYVVDVDSWGTYPRTG 120
Qy 121 TYKGTVKSDDGTYDYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGNSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKRYGMNLGSNWYQVLATEGYRSGSSNVTW 213

RESULT 7

US-11-170-653-1
; Sequence 1, Application US/11170653
; Publication No. US20050271769A1

GENERAL INFORMATION:

; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0

```
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-170-653-1

Query Match      88.9%; Score 1041; DB 7; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.5e-84;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNMSNTGNFVVGKWTGSPRTINYNAGWAP 88
Db 1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNMSNTGNFVVGKWTGSPRTINYNAGWAP 60

Qy 89 NNGYLILYGWTRSPLEIYYVVDWSWGTYPRTGTVKGVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLILYGWTRSPLEIYYVVDWSWGTYPRTGTVKGVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQVWSVRQSKRPTGNSNATITFSNHNNAWKGHGMNLGSNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQVWSVRQSKRPTGNSNATITFSNHNNAWKGHGMNLGSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVW 213
Db 181 NVTVW 185

RESULT 8
US-10-517-939-198
; Sequence 198, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Unknown
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Unknown
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-198

Query Match      81.4%; Score 953; DB 6; Length 211;
Best Local Similarity 81.7%; Pred. No. 9e-77;
Matches 174; Conservative 13; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKFKNLFVGLSAAALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKFKNMTVILAAHWSFGLF-ATTSSATDYQWNTDGGGIVNAVNGSGGNSVTVQN 59

Qy 61 TGNFVVGKWTGSPRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTG 120
Db 60 TGNFVVGKWTGSPRTINYNAGWAPNGNGYLTLYGWTRNALIEYYVVDWSWGTYPRTG 119
```

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Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGRTTFTQVWSVRQSKRPTGNSNATITFSNHVNA 180
Db 120 TYKGTVTS DGGTYDIYTTMEHNAPSIDGTQ-TFAQYWSVRQSKRATGVNSSITFSNHVNA 178

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 179 WASKGMNLGSSWSYQVLATEGYQSSGSSNVTVW 211

RESULT 9
US-10-517-939-158
; Sequence 158, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
US-10-517-939-158

Query Match      79.7%; Score 933.5; DB 6; Length 214;
Best Local Similarity 80.4%; Pred. No. 4.6e-75;
Matches 172; Conservative 12; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MFKFKNLFVGLSAAALMS-ISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWS 59
Db 1 MFKLSKKILAVLLTISMSFSLFAVTAYAASTDYQWNTDGGGTVNATNGSDGNSVWS 60

Qy 60 NTGNFVVGKWTGSPRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGTYPRT 119
Db 61 NCGNFVVGKWTGSAATRVINYNAGAFSPSGNGYALYGTWTRNSLIEYYVVDWSWGTYPRT 120

Qy 120 GTYKGTVKS DGGTYDIYTTTRYNAPSIDGRTTFTQVWSVRQSKRPTGNSNATITFSNHVN 179
Db 121 GTYKGTVTS DGGTYDIYTTTTRTNAPSIDGNNTFQFWSVRQSKRPIGTNNITITFSNHVN 180

Qy 180 AWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 181 AWKSKGMNLGSSWAYQVLATEGYQSSGSSNVTVW 214

RESULT 10
US-11-170-653-19
; Sequence 19, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
```

```
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 211
; TYPE: PRT
; ORGANISM: A. caviae
US-11-170-653-19

Query Match      79.3%; Score 929; DB 7; Length 211;
Best Local Similarity 79.3%; Pred. No. 1.le-74;
Matches 169; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKEKFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKEGKMLMTVLAAASMGVFAATSSAA-TDYQNWNTDGGGTVNAVNGSGGNYSVSQN 59

Qy 61 TGNFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 60 TGNFVVGKWTGYTPNRVNVNAGVAFSPGNGYLTLYGWTRNALIYYVVDVSWGTYRPTG 119

Qy 121 TYGTVKSDGGTYDIYTTTTRYNAPSIDGDRFTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
Db 120 TYGTVNSDGGTYDIYTTTMRYNAPSIDGTQ-TFPQYWSVRQSKRPTGVSNTITFSNHVNA 178

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 179 WPSKGMVNLGSWSYQVLAATEGYQSSGSNANVTW 211
```

```
RESULT 11
US-10-517-939-208
; Sequence 208, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
US-10-517-939-208
```

```
Query Match      79.2%; Score 927; DB 6; Length 210;
Best Local Similarity 80.1%; Pred. No. 1.7e-74;
Matches 169; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

Qy 3 KFKKNFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGIVNAVNGSGGNYSVNWSNTG 62
Db 2 KLKKMLTLLLTASMSFGLFGATSSAA-TDYQWQWTDGGGIVNAVNGSGGNYSVTWQNSG 60

Qy 63 NFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGY 122
Db 61 NFVVGKWSVGPRTINYNAGIWEPSGNGYLTLYGWTRNSLIEYYVVDVSWGTYRPTGTH 120

Qy 123 KGTVKSDDGGTYDIYTTTTRYNAPSIDGDRFTFTQYWSVRQSKRPTGSGNATITFSNHVNAWK 182
Db 121 KGTVNSDGGTYDIYTTTMRYNAPSIDGTQ-TFQFWSVRQSKRPTGSGNVSIITFSNHVNAWR 179

Qy 183 SHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 180 SKGMNLGSSWSYQVLAATEGYQSSGSRSNVTW 210

RESULT 12
US-11-170-653-18
; Sequence 18, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-11-170-653-18
```

```
Query Match      77.5%; Score 907.5; DB 7; Length 211;
Best Local Similarity 79.2%; Pred. No. 8.6e-73;
Matches 168; Conservative 12; Mismatches 29; Indels 3; Gaps 3;

Qy 3 KFKKNFLVGLSAAALMSISLFSATASASTDYQNWNTDGGGIVNAVNGSGGNYSVNWSNTG 62
Db 2 KLKKMLTLLLTASMSFGLFGATSSAA-TDYQWQWTDGGGIVNAVNGSGGNYSVTWQNTG 60

Qy 63 NFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGY 122
Db 61 NFVVGKWTGSPNRVINYNAGIWEPSGNGYLTLYGWTRNALIYYVVDVSWGTYRATONY 120

Qy 123 K-GTVKSDGGTYDIYTTTTRYNAPSIDGDRFTFTQYWSVRQSKRPTGSGNATITFSNHVNAW 181
Db 121 ESGTVNSDGGTYDIYTTTMRYNAPSIDGTQ-TFQFWSVRQSKRPTGSGNVSIITFSNHVNAW 179

Qy 182 KSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 180 RSKGMNLGSSWAYQVLAATEGYQSSGSRSNVTW 211
```

```
RESULT 13
US-10-517-939-190
```

```
; Sequence 190, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-517-939-190

Query Match 75.7%; Score 886; DB 6; Length 189;
Best Local Similarity 84.0%; Pred. No. 5.8e-71;
Matches 158; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 26 ASAASTDYQWNTDGGGIVNAVSGGNYSYNWSNTGNFVVGKGTGSPRTINYNAGV 85
Db 2 ALMASTDYQWNTDGGGIVNAVSGGNYSYNWSNCGNFVVGKGTGTSATRVYNAGA 61

Qy 86 WAPNGCYLYGWTRSPLEIYYVVDSWGTYRPTGTYKGTVDGGTYDIYTTTRYNAPS 145
Db 62 FSPSGNGYLYGWTRNSLIYYVVDSWGTYRPTGTYKGTVDGGTYDIYTTTRYNAPS 121

Qy 146 IDGRTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKGNLGSNNWAYQVMATEGYQSS 205
Db 122 IDGNNTTFTQWSVRQSKRPIGTNTITFSNHNVAWSKGNLGSNNWAYQVMATEGYQSS 181

Qy 206 GSSNVTVW 213
Db 182 GYSNVTVW 189

RESULT 14
US-10-517-939-252
; Sequence 252, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0

; Sequence 190, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0

; Sequence 380, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 380
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated polypeptide.
US-10-517-939-380

Query Match 72.1%; Score 844; DB 6; Length 189;
Best Local Similarity 81.4%; Pred. No. 2.8e-67;
Matches 153; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

Qy 26 ASAASTDYQWNTDGGGIVNAVSGGNYSYNWSNTGNFVVGKGTGSPRTINYNAGV 85
Db 2 ALMASTDYQWNTDGGGIVNAVSGGNYSYNWSNCGNFVVGKGTGTSATRVYNAGA 61

Qy 86 WAPNGCYLYGWTRSPLEIYYVVDSWGTYRPTGTYKGTVDGGTYDIYTTTRYNAPS 145
Db 62 FSPVGNAYLALYGWTRNSLIYYVVDSWGTYRPTGTYKGTVDGGTYDIYTTTRYNAPS 121

Qy 146 IDGRTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKGNLGSNNWAYQVMATEGYQSS 205
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Db 122 IDGNITTFQFWSVRQSRPIGTNTTTFSSHVNAWKSQGNLGSNSYQVLAEGYOSS 181

Qy 206 GSSNVTW 213

Db 182 GYSNVTW 189

Search completed: February 3, 2006, 09:13:20
Job time : 8 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:12:23 ; Search time 79 Seconds
(without alignments)
1126.552 Million cell updates/sec

Title: US-10-626-724-5
Perfect score: 1171
Sequence: 1 MFKFKNFLVGLSALMSIS.....YQVMATEGYQSSGSNTVTW 213

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	100.0	213	4	US-10-237-386-16
2	1171	100.0	213	5	US-10-626-583-5
3	1171	100.0	213	5	US-10-626-724-5
4	1168	99.7	213	4	US-10-237-386-17
5	1161	99.1	213	5	US-10-626-583-11
6	1161	99.1	213	5	US-10-626-724-11
7	1154	98.5	213	5	US-10-626-583-7
8	1154	98.5	213	5	US-10-626-724-7
9	1149	98.1	213	5	US-10-626-583-9
10	1149	98.1	213	5	US-10-626-724-9
11	1130	96.5	213	5	US-10-626-583-3
12	1130	96.5	213	5	US-10-626-724-3
13	1041	88.9	185	4	US-10-307-441-5
14	1041	88.9	185	4	US-10-237-386-1
15	1041	88.9	185	6	US-11-088-725A-32
16	1041	88.9	197	4	US-10-442-148A-10
17	1041	88.9	360	4	US-10-442-148A-11
18	1038	88.6	185	4	US-10-307-441-3
19	1038	88.6	185	6	US-11-088-725A-30
20	929	79.3	211	4	US-10-237-386-19
21	907.5	77.5	211	4	US-10-237-386-18
22	885	75.6	185	6	US-11-018-645-2
23	885	75.6	186	6	US-11-018-645-14
24	826.5	70.6	192	6	US-11-018-645-8
25	825	70.5	186	6	US-11-018-645-16
26	686.5	58.6	197	6	US-11-018-645-4
27	686.5	58.6	198	6	US-11-018-645-18

28	663.5	56.7	241	4	US-10-237-386-43	Sequence 43, Appl
29	659	56.3	240	4	US-10-237-386-42	Sequence 42, Appl
30	646	55.2	242	4	US-10-237-386-41	Sequence 41, Appl
31	645.5	55.1	239	4	US-10-237-386-40	Sequence 40, Appl
32	640.5	54.7	189	4	US-10-307-441-13	Sequence 13, Appl
33	640.5	54.7	189	6	US-11-088-725A-40	Sequence 40, Appl
34	636	54.3	344	3	US-09-770-621-2	Sequence 2, Appl
35	636	54.3	344	4	US-10-286-993-2	Sequence 2, Appl
36	627.5	53.6	191	6	US-11-088-725A-44	Sequence 44, Appl
37	622	53.1	228	4	US-10-237-386-39	Sequence 39, Appl
38	621	53.0	240	4	US-10-237-386-38	Sequence 38, Appl
39	618.5	52.8	191	4	US-10-307-441-11	Sequence 11, Appl
40	618.5	52.8	191	6	US-11-088-725A-39	Sequence 39, Appl
41	617.5	52.7	234	4	US-10-213-990-69	Sequence 69, Appl
42	587	50.1	191	4	US-10-307-441-10	Sequence 10, Appl
43	587	50.1	191	6	US-11-088-725A-38	Sequence 38, Appl
44	581	49.6	225	4	US-10-237-386-36	Sequence 36, Appl
45	573.5	49.0	189	4	US-10-307-441-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-237-386-16
; Sequence 16, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-16

Query Match	100.0%	Score 1171;	DB 4;	Length 213;
Best Local Similarity	100.0%	Pred. No. 1.5e-96;		
Matches 213;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFKFKNFLVGLSALMSISLFSATASASTDYQNWTDGGGINAVNNGSGNSVNWNS	60	
Db	1	MFKFKNFLVGLSALMSISLFSATASASTDYQNWTDGGGINAVNNGSGNSVNWNS	60	
Qy	61	TGNFVVGKGTGTPFRITINYNAGVWAPNGNYLTLYGWTSPLEIYYVDSWGTYRPTG	120	
Db	61	TGNFVVGKGTGTPFRITINYNAGVWAPNGNYLTLYGWTSPLEIYYVDSWGTYRPTG	120	
Qy	121	TYKGTVKSDDGYDIYTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA	180	
Db	121	TYKGTVKSDDGYDIYTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA	180	
Qy	181	WKGHGMNLGNSWAYQVMATEGYQSSGSNTVTW	213	
Db	181	WKGHGMNLGNSWAYQVMATEGYQSSGSNTVTW	213	

No Dbl. rat.
c
time.

RESULT 2
US-10-626-583-5
; Sequence 5, Application US/10626583

Publication No. US20040234998A1
GENERAL INFORMATION:
APPLICANT: SIBBESEN, OLE
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 078883/0132
CURRENT APPLICATION NUMBER: US/10/626.583
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/869,155
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/IB99/02071
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: GB 9828599.2
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: GB 9907805.7
PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: GB 9908645.6
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 213
TYPE: PRT
ORGANISM: Bacillus subtilis
US-10-626-583-5

Query Match 100.0%; Score 1171; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60
DB 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60
QY 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
DB 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVA 180
QY 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 3
US-10-626-724-5
Sequence 5, Application US/10626724
Publication No. US20050079573A1
GENERAL INFORMATION:
APPLICANT: SIBBESEN, OLE
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 078883/0132
CURRENT APPLICATION NUMBER: US/10/626.724
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/869,155
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: PCT/IB99/02071
PRIOR FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: GB 9828599.2
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: GB 9907805.7
PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: GB 9908645.6
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 213
TYPE: PRT

ORGANISM: Bacillus subtilis
US-10-626-724-5
Query Match 100.0%; Score 1171; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60
DB 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60
QY 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
DB 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVA 180
QY 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 4
US-10-237-386-17
Sequence 17, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sibbesen, Ole
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 213
TYPE: PRT
ORGANISM: Bacillus circulans
US-10-237-386-17

Query Match 99.7%; Score 1168; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.8e-96;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60
DB 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGNSVNWNS 60
QY 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
DB 61 TGNFVVGKGTGSPFRTINYNAGWAPNGNGYLLYGWTRSPLEIYYVVDVDSWGTYRPTG 120
QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVA 180
QY 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 5
US-10-626-583-11

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; Sequence 11, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESENSEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-11
```

```
Query Match 99.1%; Score 1161; DB 5; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYWQNTDGGGINVAVNGSGGNYSVNWSN 60
DB 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYWQNTDGGGINVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGLYLTGWTSPLEIYYVVDVDSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGLYLTGWTSPLEIYYVVDVDSWGTYPRTG 120

QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
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RESULT 6
US-10-626-724-11
; Sequence 11, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESENSEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; NUMBER OF SEQ ID NOS: 19
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-11

Query Match 99.1%; Score 1161; DB 5; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYWQNTDGGGINVAVNGSGGNYSVNWSN 60
DB 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYWQNTDGGGINVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGLYLTGWTSPLEIYYVVDVDSWGTYPRTG 120
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGLYLTGWTSPLEIYYVVDVDSWGTYPRTG 120

QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213
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RESULT 7
US-10-626-583-7
; Sequence 7, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESENSEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR FILING DATE: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-7
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Query Match 98.5%; Score 1154; DB 5; Length 213;
Best Local Similarity 98.1%; Pred. No. 4.9e-95;
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYWQNTDGGGINVAVNGSGGNYSVNWSN 60
DB 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYWQNTDGGGINVAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGLYLTGWTSPLEIYYVVDVDSWGTYPRTG 120
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Db 61 TGNFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 8

US-10-626-724-7
; Sequence 7, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-7

Query Match 98.5%; Score 1154; DB 5; Length 213;
Best Local Similarity 98.1%; Pred. No. 4.9e-95;
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 9

US-10-626-583-9
; Sequence 9, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132

; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-9

Query Match 98.1%; Score 1149; DB 5; Length 213;
Best Local Similarity 97.7%; Pred. No. 1.4e-94;
Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWNTDGGGIVNAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPERTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRSQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 10

US-10-626-724-9
; Sequence 9, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

Qy	1	MFKPKNFLVCLSAALMSILFSATASAASTDYWNNTDGGGINAVNGSGGNYSVNWSN	60
Dd	1	MEFKKKFLVGLTAAFMISIMFSATASAASTDYWNNTDGGGTNAVNGSGGNYSVNWSN	60
Qy	61	TGNFVKGWKMTGSPFTTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDSWGTYRPTG	120
Dd	61	TGNFVKGWKMTGSPFTTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDSWGTYRPTG	120
Qy	121	TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTFYQYWSVRQSKEPTGSNATIFESNVNA	180
Dd	121	TYKGTVKSDGGTYDIYTTTRYNAPSIDGDNFTFYQYWSVRQSKEPTGSNAAITFSNVNA	180
Qy	181	WKSHGMNLGSNWAYQMATEGYQSSGSSNTVTW	213

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; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-307-441-5

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTINYNAGVWAP 88
Db 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTINYNAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNNAWKGHGMNLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNNAWKGHGMNLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 14
US-10-237-386-1
; Sequence 1, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-1

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTINYNAGVWAP 88
Db 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTINYNAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNNAWKGHGMNLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNNAWKGHGMNLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
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RESULT 15
US-11-088-725A-32
; Sequence 32, Application US/11088725A
; Publication No. US20050214410A1
; GENERAL INFORMATION:
; APPLICANT: Iogen Bio-Products Corporation
; APPLICANT: White, Theresa C
; APPLICANT: Giroux, Genevieve R
; APPLICANT: Wallace, Katie E.A.
; TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
; FILE REFERENCE: Q80712
; CURRENT APPLICATION NUMBER: US/11/088,725A
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/556,061
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-088-725A-32
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Query Match      88.9%; Score 1041; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTINYNAGVWAP 88
Db 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTINYNAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNNAWKGHGMNLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNNAWKGHGMNLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
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Search completed: February 3, 2006, 09:13:51
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